From:

Whiteman, Brian

Sent:

Thursday, November 10, 2005 10:35 AM

To:

STIC-Biotech/ChemLib

Subject:

seq search

10/696,282 Wilson et al.

SEQ ID NO: 13, 15, and 17 and

nucleotides 335 to 2272 of SEQ ID NO: 1 and nucleotides 1007 to 2272 of SEQ ID NO: 1:

- 1) search against us issued and published us patent database
- 2) commercial databases

thank you,

Brian Whiteman Remsen, 2D14 mail box 2C18 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office (571) 272-0764

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Searcher Phone:	
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Other (Specify):

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From:

Whiteman, Brian

Sent:

Thursday, November 10, 2005 10:41 AM STIC-Biotech/ChemLib seq search

To: Subject:

10/696,900 Wilson et al.

nucleotides 1 to 143 of SEQ ID NO: 1; nucleotides 4576-4718 of SEQ ID NO: 1; nucleotides 2223-4431 of SEQ ID NO: 1; nucleotides 2829-4432 of SEQ ID NO: 1

- 1) search against us issued and published us patent database
- 2) commercial databases

thank you,

Brian Whiteman Remsen, 2D14 mail box 2C18 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office (571) 272-0764

4718 NR

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AA#: Oligomer: Encode/Transl:_ Structure #:_ Inventor:___ Litigation:

Vendors and cost where applicable Other (Specify):

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Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMARIES

Result No.	Score	% Query Match	% Query Match Length	DB	ID	Description		
	3989	100.0	736	ω	AAY71167	Aay71167 Ac	Adeno-ass	
2	3989	100.0	736	σ	ABB80232		AAV1 vp1	
ω	3989		736	7	ABR62762	Abr62762 Ad	Adeno ass	
4.	3989		736	7	ADE76565	Ade76565 Ad	Adeno-ass	
տ	3989	100.0	736	Q	ADV70294	Adv70294 Pi	Primate a	
σ	3989	100.0	736	ø	ADZ27069	Adz27069 Ad	Adeno-ass	
7	3989	100.0	736	9	ADZ27012	Adz27012 Ad	Adeno-ass	
œ	3985	99.9	735	9	ADV67506	Adv67506 An	Amino aci	
9	3968	99.5	736	9	ADZ27007	Adz27007 Ad	Adeno-ass	
10	3963		736	4	AAB59847	Aab59847 AF	AAV6 caps	
11	3963	99.3	736	7	ADE76566	Ade76566 Ad	Adeno-ass	
12	3963	99.3	736	ø	ADV70293	Adv70293 Pi	Primate a	
13	3963	99.3	736	9	ADZ27070	_	Adeno-ass	
14	3897.5	97.7	737	9	ADZ27086	Adz27086 Ac	Adeno-ass	
15	3883.5	97.4	737	ø	ADZ27010	_	Adeno-ass	
16	3883	97.3	736	9	ADZ27074	Adz27074 Ac	Adeno-ass	
17	3873	97.1	736	9	ADZ27008	_	Adeno-ass	
18	3853	96.6	736	9	ADZ27009		Adeno-ass	
19	3511	88.0	736	4	AAB59846	Aab59846 AJ	AAV3B cap	4
20	3494	87.6	736	4	AAB59845	_	AAV3A cap	.2.
21	3494	87.6	736	σ	ABB80233	Abb80233 AJ	AAV3 vp1	
22	3494	87.6	736	7	ABR62763		Adeno ass	
23	3494	87.6	736	7	ADE76572	•••	Adeno-ass	
24	3494	87.6	736	9	ADV67507	Adv67507 Ar	Amino aci	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25
3453.5	3453.5	3455.5	3456	3456.5	3456.5	3456.5	3457	3458.5	3460	3464	3464.5	3467	3467	3467	3467	3469	3473	3476	3483.5	3494
86.6	86.6	86.6	86.6	86.7	86.7	86.7	86.7	86.7	86.7	86.8	86.9	86.9	86.9	86.9	86.9	~1	7	7.	87.3	87.6
735	735	737	738	737	737	735	736	737	736	736	737	736	736	736	736	738	736	736	737	736
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ADZ26992	ADZ26996	ADZ26965	ADZ26951	ADZ26962	ADZ26966	ADZ27034	ADE76600	ADZ26963	ADE76599	ADE76597	ADZ27080	ADV67508	ADE76601	ABR62764	ABB80229	ADZ26960	ADE76598	ADZ27085	ADZ26959	ADZ27067
Adz26992	Adz26996	Adz26965	Adz26951	Adz26962	Adz26966	Adz27034	Ade76600	Adz26963	Ade76599	Ade76597	Adz27080	Adv67508	Ade76601	Abr62764	Abb80229	Adz26960	Ade76598	Adz27085	Adz26959	Adz27067
Adeno-as	Adeno-ass	Amino aci	Adeno-ass	Adeno ass	AAV9 cap	Adeno-ass	Adeno-ass	Adeno-ass	Adeno-ass	Adeno-ass										

ALIGNMENTS

RESULT 1
AAY71167
ID AAY7 Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy; vaccine; transgene; VP1. Adeno-associated virus serotype 1 capsid protein VP1. AAY71167 standard; protein; 736 AA. WO200028061-A2 08-SEP-2000 (first entry) AAY71167; 05-NOV-1998; 02-NOV-1999; 18-MAY-2000. Adeno-associated virus 1. (UYPE-) UNIV PENNSYLVANIA. 98US-0107114P 99WO-US025694.

Wilson JM, Xiao W;

WPI; 2000-376571/32. N-PSDB; AAD00772, AAD00777.

Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.

Claim 7; Page 87-90; 108pp; English.

The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a

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RESULT 2
ABB80232
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           AAV1
                              20-NOV-2003
                                                                    ABB80232
          vp1 protein
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                                                                   standard;
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                                                                                                                                                                       EFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGL
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GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGV
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                                                                                                                                                                              GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
                                                                                                                                                                                                                                                                                                                                                   TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
                                                                   FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP
                                                                                         FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP
                                                                                                                                                   GCLPPFPADVFMIPQYGYLTLINIGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
                                                                                                                                                                                                                                      INNIWGFREKRLNEKLENIQVKEVTTNDGVTTIANNLTSTVQVESDSEYQLEYVLGSAHQ
                                                                                                                                                                                                                                                              INNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
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2002US-0386132P
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Pred. No. 4.9e-311;
Mismatches 0;
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Best Local Similarity

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RESULT 3
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01-MAY-2002;
05-JUN-2002;
                                                                                  The present sequence is the protein sequence of the vpl capsid protein of adeno associated virus serotype 1 (AAVI). The invention provides the nucleic acid and amino acid sequences of novel AAV8 and fragments of these sequences. Each of these fragments may be used in a variety of vector systems and host cells. Among the desirable fragments are the cap proteins, including vpl, vp2, vp3 and hypervariable regions, the rep proteins, including vpl, vp2, vp3 and hypervariable regions, the rep proteins, including rep78, rep68, rep52 and rep40, and the sequences encoding these proteins. The fragments may be used alone, in combination with other AAV8 sequences or in combination with elements from other AAV0 or non-AAV viral sequences in the production of recombinant AAV and for use as antisense delivery vectors, gene therapy vectors or vaccine vectors. A claimed molecule comptises a cap protein of a functional AAV rep gene from a serotype selected from AAV1, AAV2, AAV3, AAV4, AAV5 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence of AAV8, useful for preparing a medicament for delivery of a transgene to a cell and for treating cystic fibrosis or hemophilia B.
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AAV6
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2002US-0377133P
2002US-0386122P
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                      adeno-associated virus; AAV; cytostatic; antipsoriatic; an antiarthritic; neuroprotective; antidiabetic; antithyroid; dermatological; antiinflammatory; gene therapy; vaccine; hyperproliferative; cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
                                                                                              Adeno-associated virus (AAV)
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17-DEC-2001;
01-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antipsoriatic, antipheumatic, antiarthritic, neuroprotective, antidiabetic, antithyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This sequence represents an AAV related protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing or treating hyperproliferative or a comprises subjecting a sample having a DNA to polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via
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                                                                                                                                                                                    SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI
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                                                              INNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
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                                              INNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
                                                                                                       TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
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2002US-0386675P.
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Pred. No. 4.9e-311;
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30-APR-2004;
03-JUN-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive; gene therapy; immunogenicity; virus inactivation; hemophilia; Pepck deficiency; galactosemia; phenylketonuria; Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia; atherosclerosis; thrombosis; embolism; Parkinson's disease; congestive heart failure; cancer; inflammation; immune disorder; muscular dystrophy; diabetes; VP1.
                                                                                                                                                                           New mutated adeno-associated virus (AAV) capsid protein that when pin an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding wild-type virion, useful for treating hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-2004;
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The invention describes a mutated adeno-associated virus (AAV) of protein that when present in an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding

described are: a polynucleotide encoding

the mutated

capsid wild-type ed protein

6.9.

SEQ

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English

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CC above; a recombinant AAV virion comprising the mutated protein above; and CC delivering a recombinant AAV virion to a cell or tissue of a vertebrate CC subject. The recombinant AAV virion is useful for delivering a CC heterologous nucleic acid molecule to a cell or tissue of a vertebrate CC subject, where the protein encoded by the heterologous nucleic acid molecule is expressed at a level that provides a therapeutic effect, CC where the recombinant AAV virion may comprise a non-primate, mammalian CC immunoreactivity to the virion as compared to immunoreactivity of primate of control encodes a therapeutic primate decreased in control elements capable of directing the in vivo transcription cC in useful for treating or preventing a wide variety of disorders such as thempohila, glycogen storage deficiency type 1A, pepck deficiency, CC galactosemia, phenyletonuria, Crigler-Najjar disease, Gout and Lesch-CC Nyan syndrome, Zellweger syndrome, ischemic diseases, atherosclerosis, CC cancer, inflammatory and immune disorders, muscular dystrophies, and CC diabetes. This is the amino acid sequence of adeno-associated virus 1 crigler-Naj and control expection vivo.
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                                                                                                                                                                        MIFGKESAGASNTALDNYMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
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                                                                                                                                                                                                                                                                           GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAWASHKDDEDKFFPMSGV
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EFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGL
                                              ALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPA 660
                                                                                                                                                 MIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG
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KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ

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                                                                                                                                  The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarthritic; neuroprotective; antiinflammatory; antiidabetic; antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; virucide; antibacterial; cytostatic; antiulcer; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; bacterial infection; cancer; ulcerative colitis; antirhumatic;
                                                                                                                                                                                                                                                                                                                                                New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
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                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 219; 569pp; English.
                                                                                                                                                                                                                                                                                                                                  sclerosis, diabetes, scleroderma, infection and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-2003; 2003US-0508226P.
29-APR-2004; 2004US-0566546P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adeno-associated virus.
                                                                                                           Sequence
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Gao G,
                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Alvira MR,
                                                                   100.0%;
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                                                      0;
                                                     Score 3989; DB 9;
Pred. No. 4.9e-311;
Mismatches 0;
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30-SEP-2003; 2003US-0508226P
                           30-SEP-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of adeno-associated virus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New adeno-associated virus (AAV) clade comprising at least three members, useful for preventing and/or treating arthritis, multipscierosis, diabetes, scieroderma, psoriasis, hemophilia, HIV, ba
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                          GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGV
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                                                                                         FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP
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                                                                         FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP
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                                                                                                                                                                                                                                                                 The specification describes a method for lowering total cholesterol levels in a subject. The method comprises delivering to the subject a recombinant adeno-associated virus (AAV) comprising a gene encoding a human apolipoprotein E (apoB) or apoA under the control of a regulatory control sequence which directs expression of the gene. The recombinant AAV also comprises a capsid protein selected from an AAV serotype (e.g. AAV7) or AAV8) which preferentially expresses high levels of transgene in live. A therapeutically effective amount of apoE or apoA expression is obtained upon delivery of low dose of AAV. The method of the invention is useful for lowering total cholesterol levels in a subject, e.g. for treating atherosclerosis, and for correcting defects in lipoprotein. The present sequence represents a cappid protein of AAV serotype 1 (AAV1), which may be used in recombinant AAV vectors of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lowering total cholesterol levels and treating atherosclerosis in subject comprises delivering a recombinant adeno-associated virus comprising an AAV serotype capsid protein or a gene encoding human apolipoprotein E (apoE) or apoA.
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apolipoprotein E; apoE; apolipoprotein A; apoA; atherosclerosis;
lipoprotein defect; capsid protein.
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                                                                                                         Local Similarity
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ive 0; Mismatches 0
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rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antirheumatic; antipatritic; neuroprotective; antiinflammatory; antidiabetic; antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological.

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Adeno-associated virus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 736 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial infection and cancer.
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29-APR-2004;
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                                                    GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGV
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                               GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESI INPGTAVASHKDDEDKFFPMSGV
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 MIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG
                                                                                             FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP
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2004US-0566546P.
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Pred. No. 2.4e-309;
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RESULT 10
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Matches
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                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 syndrome, sickle cell anemia, thalassemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adeno-associated virus serotype 6 and viral vector derived from it gene therapy of cystic fibrosis, cancer, acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-060164/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-1997;
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GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVP GCLPPFPADVEMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP INNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ INNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL

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Query Match
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Matches 730
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17-DEC-2001;
01-MAY-2002;
05-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antidisbetic, antirheumatic, antiarthritic, neuroprotective, antidisbetic, antithyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This sequence represents an AAV related protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR) The AAV sequence have the following activities: cytostatic,
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TTSTRTWALFTYNNHLYKQISSASTGASNDNHYFGYSTFWGYFDFNRFHCHFSPRDWQRL
                                                                   SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI
                                                                                            SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI
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2001US-0341117P.
2002US-0377066P.
2002US-0386675P.
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No. 6.1e-309;
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The invention describes a mutated adeno-associated virus (AAV) capsid protein that when present in an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding wild-type virion. Also described are: a polymucleotide encoding the mutated protein above; a recombinant AAV virion comprising the mutated protein above; and delivering a recombinant AAV virion to a cell or tissue of a vertebrate subject. The recombinant AAV virion is useful for delivering a heterologous nucleic acid molecule to a cell or tissue of a vertebrate subject, where the protein encoded by the heterologous nucleic acid molecule is expressed at a level that provides a therapeutic effect, where the recombinant AAV virion may comprise a non-primate, mammalian AAV capsid protein that when present in an AAV virion imparts decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressive; gene therapy; immunogenicity; virus inactivation; hemophilia, Pepck deficiency; galactosemia; phenylketonuria; Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia; atherosclerosis; thrombosis; embolism; Parkinson's disease; congestive heart failure; cancer; inflammation; immune disorder;
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30-APR-2004; 2004US-0567310P
03-JUN-2004; 2004US-0576501P
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                                                                                                                                                                                                                                                                                                     disease, hemophilia, hiv, pauretta ...... colitis. The present sequence represents adeno-associated virus protein.
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virucide; antibacterial; cytostatic; antiulcer; dermatological.
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29-APR-2004; 2004US-0566546P.
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29-APR-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRV
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                                                                                                                                                                                                         VMIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAM
                                                                                                                                                                                                                                                                                            PGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSG
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AEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSASVDFTVDNNG
                                                                                                                                                                                                                                                                  PGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESI INPGTAMASHKDDEDKFFPMSG
                                                                                                                                                                                                                                                                                                                                                   PLHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWL
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HIV, bacterial
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                                                                                                                                                                                                                                                                             The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis,
                                                                                                                                                                                                                                      sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antiinfammatory; antidabetic; antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV; antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
                                                                                                                                                                                                Sequence
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29-APR-2004;
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 AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS
                                                         KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
                                                                                                                                                                                                 737
                             KGEPVNAADAAALEHDKAYDQQLKAGDNPYPRYNHADAEFQERLQEDTPFGGNLGRAVFQ
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2004US-0566546P
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                                                                                                                                         Score 3883.5; DB y;
Pred. No. 1.5e-302;
Pred. No. 1.5e-302;
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721 LYTEPRP	720 LYTEPI	661 AEFSA	660 AEFSA:	601 GALPGN	600 GALPGN	541 VMIFGE	540 VMIFGE	481 PGPCYF	480 PGPCYF	421 PLHSS	420 PFHSSY	361 QGCLPF	360 QGCLPE	301 LINNNW	300 LINNNW	241 ITTSTR	240 ITTSTR	181 ESVPDE	180 ESVPDF	121 AKKRVI
PIGTRYLTRPL 737	LYTEPRPIGTRYLTRPL 736	AEFSATKFASFITQYSTGQVSVE	AEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNG	GALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPP	GALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPP	VMI FGKESAGASNTALDNVM	VMIFGKESAGASNTALDNVMITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAM	PGPCYRQQRVSKTKTDNNNSNPTWTGASKYNLNGRESIINPGTAMASHKDDEDKFPPMSG	PGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSG	PLHSSYAHSQSLDRLMNPLIVQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWL	PFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWL	QGCLPPFPADVEMI PQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEV	QGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFFSYTFBEV	LINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAH	LINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAH	TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQR	TTSTRTWALFTYNNHLYKQISSASTGASNDNHYFGYSTFWGYFDFNRFHCHFSPRDWQR	ESVPDPQPIGEPPAGPSGLGSGTMAAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRV	ESVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRV	
7	66	H-	SVEIEWELOKENSK	AKIPHTDGHFHPSP	AKIPHTDGHFHPSP	ITDEEEIKATNPVA	ITDEEEIKATNPVA	NETWIGASKYNLNG	NETWTGASKYNLNG:	ZYLYYLNRTQNQS)QYLYYLNRTQNQS(CLNNGSQAVGRSSF	TLNNGSQAVGRSSF	OVKEVTTNDGVTTI	OKEVTTNDGVTTI	SSASTGASNDNHY	[SSASTGASNDNHY]	GTMAAGGGAPMADI	TTMASGGGAPMADI	KKRPVEPSPQRSPI
		EWELOKENSKRWNPEVOYTSNYAKSASVDFTVDNNG	RWNPEVQYTSNYAK	LMGGFGLKNPPPQI	LMGGFGLKNPPPQI	NTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAM	TERFGTVAVNFQSS	RESIINPGTAMASH	RESIINPGTAMASH	SAQNKDLLFSRGS	3SAQNKDLLFSRGS	CLEYFPSQMLRTG	CLEYFPSQMLRTG	ANNLTSTVQVFSDS	ANNLTSTVQVFSDSI	GYSTPWGYFDFNR	GYSTPWGYFDFNR	NEGADGVGNASGN	NEGADGVGNASGN	: SSTGIGKKGQQPA
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		720	719	660	659	600	599	540	539	480	479	420	419	360	359	300	299	240	239	180

Search completed: November 23, 2005, 17:35:10 Job time : 134.527 secs



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Result
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weldong
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 736
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Best Local Similarity
Matches 736; Conserv
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301 INNNWGFREKELNEKLENIQVKEVTTINDGVTTIANNLTSTVQVFSDSEYQLEYVLGSAHQ
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; ORGANISM: AAV-1
US-09-807-802A-13
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TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 736
TYPE: DET
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Best Local Similarity
Matches 736; Conserv
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SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI
                                                                             AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09321589
Patent No. 6498244
GENERAL INFORMATION:
APPLICANT: PATEL, SALIL D.
APPLICANT: MCARTHUR, JAMES G.
APPLICANT: MCARTHUR, JAMES G.
TILE REFERENCE: 39672
FILE REFERENCE: 39672
CURRENT APPLICATION NUMBER: US/09/321,589
CURRENT PILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                         Best Local
Matches 61
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                            AKKRVLEPLGLYEEGAKTAPGKKRPVEQSPOEPDSSSGIGKTGQQPAKKRLNFGQTGDSE 180
                                                                                            KGEPVNAADAAALBHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
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       AKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD
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GENERAL INFORMATION:
APPLICANT: PATEL, SALIL D.
APPLICANT: MCARTHUR, JAMES G.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CA
FILE REFERENCE: 39672
CURRENT APPLICATION NUMBER: US/10/293,478
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/321,589
PRIOR FILING DATE: 1999-05-28
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US-10-293-478-1
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 735
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                                                                                                             Query Match
Best Local Similarity
Matches 613; Conserv
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KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
                                                                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
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                                                   <u>MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD</u>
                                                                                                           85.3%; Score 3402.5; DB 2; llarity 83.3%; Pred. No. 7.2e-290; Conservative 51; Mismatches 71;
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                                                                                                                                          APPLICANT: J. Bartlett
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 735
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application Patent No. 6962815 GENERAL INFORMATION:
                                                      Matches
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                                                                                                                                 ORGANISM: adeno-associated virus 2 VP1 caspid
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                                                    85.3%; Score 3402.5;
83.3%; Pred. No. 7.2e
tive 51; Mismatches
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7.2e-290;
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RESULT 6
US-09-807-802A-15
; Sequence 15, Application US/09807802A
; Patent No. 6759237
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same

FILE REFERENCE: GNVPN.031USA

CURRENT APPLICATION NUMBER: US/09/807,802A

CURRENT FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR FILING DATE: 1998-11-05

PRIOR APPLICATION NUMBER: PCT/US99/25694

PRIOR TILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

SEQ ID NO 15

LENGTH: 599

TYPE: PRT

ORGANISM: AAV-1
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                           ; TYPE: PRT; ORGANISM: AAV-1
US-09-807-802A-17
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US-09-807-802A-17
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                                                                                                                APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNUPN 031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: DCT/US99/25694
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
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100.0%; Pred. No. 1.1e-276;
     72.9%;
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     Score 2906; DB 2;
Pred. No. 1.8e-246;
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                           Length 534;
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GENERAL INFORMATION:

APPLICANT: J. Bartlett

TITLE OF INVENTION: AAV VECTORS AND METHODS

FILE REFERENCE: 28335/36996US

CURRENT APPLICATION NUMBER: US/10/038,972A

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: US 60/260,124

PRIOR APPLICATION NUMBER: US 60/260,124

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.1

SEQ ID NO 14

LENGTH: 598

TYPE: PRT

ORGANISM: adeno-associated virus 2 VP2 capsid protien
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US-10-038-972A-14
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Best Local (
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                                                                                                                                                                                                  9.2%; Score 2759.5; DB 2; Local Similarity 82.8%; Pred. No. 1.7e-233; hes 495; Conservative 43; Mismatches 59;
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QISSASTGASNDNHYFGYSTÞWGYFDFNRFHCHFSÞRDWQRLINNNWGFRÞKRLNFKLFN 318
                                                                                                                                            APGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDDPQPLGEPPATPAAV 198
                                                         GTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNHLYK
                                                                           GPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALFTYNNHLYK 258
                                                                                                                            APGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGL 61
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APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THER
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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US-09-532-594B-4
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TYPE: PRT
ORGANISM: Artificial S
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSVEIEWELQXENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736
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                             RVLEPLGLVEQAGETAPGKKRPLIESPQQPDSSTGIGKKGKQPAKKKLVFEDETGAGDGP
                                                   RVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNF-GQTGDSESV 182
                                                                                                                  PVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKK 123
                                                                                                                                                                 DGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQOKQDDGRGLVLPGYKYLGPFNGLDKGE
                                                                                                PVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQQRLQGDTSFGGNLGRAVFQAKK
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                         Score 2486.5; DB 2; pred. No. 2.3e-209; 1; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence;
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GENERAL INFORMATION:
APPLICANT: J. BATTlett
APPLICANT: J. BATTlett
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 2835/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
SOFTMARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 533
TYPE: PAT
ORGANISM: adeno-associated virus 2 VP3 capsid protien
US-10-038-972A-15
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US-10-038-972A-15
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; Sequence 15, Application Uf
; Sequence 15, Application Uf
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                                  263 ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 322
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                                                                                                     MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNWGFRPKRLNPKLFNIQVKEVTTINGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSLLWAPDAAGKYTEPRAIGTRYLTHHL 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIEMELQKENSKRWNPEVQYTSNYAKS 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLPTVDRLTALGAVPGMVWQNRDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKHPPPQIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQN----QSGSAQNKDLLFSRGSPAGMSVQP
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                                                                                                                                                        Conservative
                                                                                                                                                                      62.2%; Score 2481.5; 83.3%; Pred. No. 3.7
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                                                                                                                                                        Mismatches
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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Kotin, Robert M.
APPLICANT: Davidson, Elizabeth
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
ITILE OF INVENTION: AAV5 VECTOR FOR TRANSDUCING BRJ
FILE REFERENCE: 14014,0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
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US-09-533-427-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 4
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09533427 Patent No. 6855314
                                                                                                                                                                                                                                                                                Matches 431;
                                                                                                                                                                                                                                                                                              Query Match
Best Local
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WTGATKYHLNGRDSLVNPGPAMASHKDDEEKFFPQSGVL1FGKQGSEKTNVD1EKVM1TD
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QLQIPAQPASSLGADTMSAGGGGPLGDNNQGADGVGNASGDWHCDSTWMGDRVVTKSTRT
                  LGEPPATPA-AVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRT 246
                                                                                                PLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQP
                                                                                                                                                        ADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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                                                                    PFGLVEEGAKTAPTGKRIDDHFPKRKKART-----EEDSKP----STSSDAEAGPSGSQ 176
                                                                                                                                      ADEVAREHDISYNEQLEAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAVFQAKKRVLE
                                                                                                                                                                                                                                           PDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                                                                                                                                                           PDWLEE-VGEGLREFLGLEAGPPKPKPNQQHQDQARGLVLPGYNYLGPGNGLDRGEPVNR 66
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                              58.6%;
                                                                                                                                                                                                                                                                              81; Mismatches
                                                                                                                                                                                                                                                                                Score 2220; DB 2;
Pred. No. 5.8e-186;
31; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.0
                                                                                                                                                                                                                                                                                                                                                                                     Sequence:/No.
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                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                 Indels
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AND

LUNG

CELLS

419 622 359

479 682 502

299

442 179

239

6855314e

26;

Gaps

67

236

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APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 598
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                      Matches
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e OTHER INFORMATION: synthetic construct NAME/KBY: misc_feature OTHER INFORMATION: AAV4 capsid protein VP2 -09-532-594B-16
                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PADVFMIPQYGYLTLN--NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSBYQLPYVLGSAHQGCLPPF
                                           TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNF-GQTGDSESVPDPQPLGEPPATPA 196
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 AVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHL
                               TAPGKKRPLIESPQQPDSSTGIGKKGKQPAKKKLVFEDETGAGDGPPEGSTSG-----A
                                                                                      Conservative
                                                                                     45.9%; Score 1830.5; DB 2; 57.8%; Pred. No. 7.2e-152; ative 74; Mismatches 154;
                                                                                      Indels 31;
                                                                                                              Length 598;
                                                                                      Gaps
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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
TITLE OF INVENTION: AAVS VECTOR FOR TRANSDUCING BRAFILE OF INVENTION NUMBER: US/09/533,427
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
ELENGTH: 508
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US-09-533-427-5
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                                                                                                          US-09-533-427-5
                                        Query Match
Best Local Similarity 55.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09533427
Patent No. 6855314
GENERAL INFORMATION:
                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                           TYPE: PRT
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                        140 PGKKREVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPA-AV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 MSDDSEMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGHVTTTSTRTWVLPTVNNHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPRAIGTRYLTHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPRPIGTRYLTRPL 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYT
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  PKRKKARTEEDSKPSTSS
                                                                                                                   Description of Artificial synthetic construct
                                                                 42.6%;
                                                     64;
                                                     Score 1700.5; DB 2;
Pred. No. 1.9e-140;
4; Mismatches 173;
                                                                                                                                    Sequence:/No.
                                                                                                                                                                                                                                                                                      BRAIN CELLS
  -DAEAGPSGSQQLQIPAQPASSL
                                                       Indels
                                                                               Length
                                                                                                                                                                                                                                                                                       AND
                                                                                                                                      6855314e
                                                       35,
                                                                                                                                                                                                                                                                                       LUNG
                                                        Gaps
                                                                                                                                                                                                                                                                                       CELLS
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APPLICANT: Davidson, Beverly
III'LE OF INVENTION: AAVA VECTOR AND USES THEREOF
FILE REFERENCE: 14014.025202
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 544
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-532-594B-18
; Sequence 18, Application
; Patent No. 6468524
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                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                              Matches
                                                            Query Match
Best Local Similarity
                                                                                                     ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: synthetic construct
NAME/KEY: misc_feature
OTHER INFORMATION: AAV4 capsid protein VP3
-09-532-594B-18
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chorini, John A. APPLICANT: Kotin, Robert M. APPLICANT: Safer, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      525
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                                                          42.4%; Score 1690.5;
59.4%; Pred. No. 1.3;
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                                              65; Mismatches
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                                                             5; DB 2;
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ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 322

MSAGGGGPLGDNNQGADGVGNASGDWHCDSTWMGDRVVTKSTRTWVLPSYNNHQYREIKS

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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
TITLE OF INVENTION: AAVS VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS
FILE REFERENCE: 14014.0323U2
FILE REFERENCE: 14014.0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 532
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09533427 Patent No. 6855314
                                                                                        Query Match
                                                       Matches
                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:/No.OTHER INFORMATION: synthetic construct
                                                                      Local Similarity
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203 MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNTSQQQTDRNAFYCLEYFPSQMLRTGNNFEITYSFEKVPFHSMYAHSQSLDRLMNPLID
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                                                 41.7%; Score 1665; DB 2; 58.9%; Pred. No. 2.1e-137; bive 54; Mismatches 154;
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YLTRPL 532	473 GQVTVEMEWELKKENSKRWNPEIQYTNNYNDPQFVDFAPDSTGEYRTTRPIGTRYLTRPI	4.	밁
YLTRPL 736	.	Ø,	S
ITQYST 472	414 PIWAKIPETGAHFHPSPAMGGFGLKHPPPMMLIKNTPVPGN-ITSFSDVPVSSFITQYST	4.	뮍
ITQYST 676	617 PIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYST	6	Ş
DVYLQG 413	354 NMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQEIVPGSVMMERDVYLQG	ų	밁
DVXTOG 616	557 NVMITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQG	5	Ş
ATYLEG 353	294 VSAFATTNRMELEGASYQVPPQPNGMTNNLQGSNTYALENTMIFNSQPANPGTTATYLEG	2	망
ALD 556	500 NFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD	5	Ş
GVNRAS 293	41 QYLYRFVSTNNTGGVQFNKNLAGRYANTYKNWFPGPMGRTQGWNLGSGVNRAS	241	망
TDNNNS 499	QYLYYLNRTQNQSGSAQNI	441	Ş
ANPLVD 240	31 RDNTENPTERSSFFCLEYFPSKWLRTGNNFEFTYNFEEVPFHSSFAPSQNLFKLANPLVD	181	Вb
MNPLID 440	NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAH	383	ફ
GYATLN 180	EVTVQDSTTTIANNLTSTVQVFTDDDXQLPYVVGNG	121	뭥
GYLTLN 382	EVTTNDGVTTIANNLTSTVQVFSDSEYQ	323	Ş
 FNIQVK 120	61 GSVDGSNANAYFGYSTPWGYFDFNRFHSHWSPRDWQRLINNYWGFRPRSLRVKIFNIQVK		망

Search completed: November 23, 2005, 17:42:46 Job time : 36.4724 secs



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DT 01-NOV-1999 (TrEMBLrel. 12,
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DT 01-MAR-2004 (TEMBLrel. 26,
DT 01-MAR-2004 (TEMBLrel. 26,
DE Capsid protein.
OS Adeno-associated virus 1.
OC Viruses; ssDNA viruses; Par
OX NCBI_TAXID=85106;
RN (1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99214338; PubMed=10
RA Xiao W., Chirmule N., Berta
RT "Gene therapy vectors based
RL J. Virol. 73:3994-4003(1999)
DR SEMBL, AF063497, AAD27757.1;
DR SMR; O9WBB; 217-736.
DR GO; GO:0005198; F:structura
DR GO; GO:0005198; F:structura
DR Ffam; pF00740; Parvo_coat;
SQ SEQUENCE 736 AA; 81375 M
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L J. Virol. 73:3994-4003(1999).

R EMBL, AF663497; AAD27757.1; -; Genomic_DNA.

R SMR; O9WBPB; 217-736.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:001908; F:structural molecule activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:001908; P:structural molecule activity; IEA.

R GO; GO:001908; P:structural molecule activity; IEA.

R GO; GO:001908; F:structural molecule activity; IEA.
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                             INNNWGFRFKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLFYVLGSAHQ
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Q6JC02_9VIRU
Q6JC47_9VIRU
Q6JC61_9VIRU
Q6JC61_9VIRU
Q6JC64_9VIRU
Q6JBZ6_9VIRU
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0005198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 736 AA; 81317 MW; 373C7C40975CD9BD
                                                                                                                                                                                                                                                                                                                     "Clades of Adeno-associated viruses are wid
tissues.";
J. Virol. 78:6381-6388(2004).
EMBL; AY530611; AAS99296.1; -; Genomic_DNA.
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Viruses; ssDNA viruses;
VCBI_TaxID=272636;
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MEDIINE=98080418; PubMed=9420229;

Rutledge E.A., Halbert C.L., Russell D.W.;

"Infectious clones and vectors derived from an (AAV) serotypes other than AAV type 2.";

J. Virol. 72:309-319(1998).

EMBL; AF028704; AAB95450.1; -; Genomic_DNA.
SNR; O56:137; 217-736.
GO; GO:0019028; F:structural molecule activit
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Q6JC13;

Q6JC13;

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C7 (Tremblrel. 2:

05-JUL-2004 (Tremblrel. 2:

05-JUL-2004 (Tremblrel. 2:

05-JUL-2004 (Tremblrel. 2:

05-JUL-2004 (Tremblrel. 2:

Capsid protein VP1.

Name=cap;

Name=cap;

Ndeno-associated virus.

Viruses; ssDNA viruses; P.

NCBI TaxID=272636;

(11)
 NUCLEOTIDE SEQUENCE.

PubMed=15163731; DOI-10.1128/JVI.78.12.6381-6388.2004;

Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
Wilson J.M.;

"Clades of Adeno-associated viruses are widely dissemir
tissues ";

J. Virol. 78:6381-6388(2004).

EMBL; AY330606; AAS99291.1; -; Genomic_DNA.
SMR; Q64C13; 218-737.

SMR; Q65C13; 218-737.
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GO; GO:0005198; F:structural molecule InterPro; IPR001403; Parvo_coat. Pfam; PP00740; Parvo_coat; 1.
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J. Virol. 78:6381-6388(2004).

EMBL; AY530607; AAS99292.1; -; Genomic_DNA.

SMR; Q6C012; 217-736.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; PARVO Coat; 1.

SEQUENCE 736 AA; 81364 MW; F2D75A06662E6376 CRC64;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo Wilson J.M.;
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                                                         EFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDPTVDNNGL
                                                                                                        ALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKWPPPQILIKWTPVPANPPA
                                                                                                                                         MIFGKESAGASNTALDNVMITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG
                                                                                                                                                                                        GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGV
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YTEPRPIGTRYLTRPL
                       YTEPRPIGTRYLTRPL
                                                                                          ALPGMVWQGRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPA
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                                              STGQVS
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RESULT 6
QGJC10 9VIRU
QGJC10 9VIRU
ID QGJC10;
AC QGJC10;
AC QGJC10;
DT 05-JUL-2004 (TrEMBLrel. 2:
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated viruses; Pace of the control of 
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Best Local Simi
Matches 711;
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GO; GO:0019028; C:viral capsid; GO; GO:0005199; F:structural mol. InterPro; IPR001403; Parvo_coat; I.

SEQUENCE 736 AA; 81388 MW; BI
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Clades of Adeno-associated viruses are widely tissues.";
J. Virol. 78:6381-6388(2004).
EMBL; AY530609; AAS99294.1; -; Genomic_DNA.
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MIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG
                                                     GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGV
                                                                                                                                                                                                                                                               GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
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                                                                                                                                                                    FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP
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                                                                                                                                               LHSSCAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNRDLLFSRGSPAGMSVQPKNWLP
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Pred. No. 7.3e-241;
9; Mismatches 16;
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MIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG

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01-JUN-1998 (TrEMBLrel. (
01-JUN-1998 (TrEMBLrel. (
01-MAR-2004 (TrEMBLrel. (
Capsid protein VP1
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MEDLINE=98080418; PubMed=9420229;
"Infectious clones and vectors derived from adeno-associated virus (AAV) serotypes other than AAV type 2.";
J. Virol. 72:309-319(1998).
EMBL; AP028705; AAB95452.1; -; Genomic_DNA.
SMR; O56139; 217-736.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; F:structural molecule activity; IEA.
InterPro; IPR001403; Parvo coat.
InterPro; IPR001403; Parvo coat.
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Viruses; ssDNA viruses;
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NCE 736 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                   SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI
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                                                                                                    GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
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                                                                       GCLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYTFEDVP
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AA; 81906 MW; DD52331AD5F0D70F CRC64;
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Pred. No. 1e-218;
8; Mismatches 57;
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EMBL; U49704; AAC55049.1; -; Genomic_DNA
SMR; Q65311; 217-736.

GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule ac
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo coat; 1.
SEQUENCE 736 AA; 81660 MW; AFF1EF47B
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Adeno-associated virus 3.
Viruses, ssDNA viruses; F
VIROSI_TaxID=46350;
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                                       TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
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86.4%; Pred. No. 1.3e-217;
tive 39; Mismatches 59;
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MEDLINE=22631657; PubMed=12716974; DOI=10.1073/pnas.0937739100;

Gao G., Alvira M.R., Somanathan S., Lu Y., Vandenberghe L.H.,

Rux J.J., Calcedo R., Sanmiguel J., Abbas Z., Wilson J.M.;

"Adeno-associated viruses undergo substantial evolution in prime
during natural infections.";

Proc. Natl. Acad. Sci. U.S.A. 100:6081-6086(2003).

Proc. Natl. Acad. Sci. U.S.A. 100:6081-6086(2003).

SMR; Q80873; 217-736.

SMR; Q80873; 217-736.

GO; GO:0019088; C:viral capsid; IEA.

GO; GO:0019089; F:structural molecule activity; IEA.
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GO:0019028; C:viral capsid; IEA.
GO:0005198; F:structural molecule activity;
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                          KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
                                                                                                       MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
  KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
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AC Q670Q8;
DT 25-OCT-2004 (TrEMBLrel. 28)
DR Name=cap;
OX Viruses; ssDNA viruses; Pa
OX Viruses; ssDNA viruses; Pa
OX NCBI TAXID=272636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cien C.L., Jensen R.L., Sc
RA Sierra T.J., Shell R., Joh
RT "Characterization of Aden
RL Submitted (JUL-2004) to th
DR SMR; Q670Q8; 217-715.
DR SMR; Q670Q8; 217-715.
DR GO; GO:005198; F:structus
DR GO; GO:005198; F:structus
DR InterPro; IPR001403; Parvo
DR Pfam; PP00740; Parvo coat;
SQ SEQUENCE 735 AA; 81887
               P NUCLEOTIDE SEQUENCE.

P NUCLEOTIDE SEQUENCE.

A Chen C.L., Jensen R.L., Schnepp B.C., Connell M.J., Bartleti
A Sferra T.J., Shell R., Johnson P.R., Clark K.R.;

"Characterization of Adeno-Associated Viruses In Children."

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

DR SMR; AY695376; AAU05370.1; -; Genomic_DNA.

DR SMR; Q67098; 217-735.

DR SMR; Q67098; C17-735.

DR GO; G0:0019028; C:viral capsid; IEA.

GO; G0:0019028; C:viral capsid; IEA.

GO; G0:0019028; C:viral capsid; IEA.

DR Hore For; IPR001403; Parvo coat; I.

DR Pfam; PP00740; Parvo coat; I.

DR Pfam; PP00740; Parvo coat; I.

SEQUENCE 735 AA; 81887 MM; 258BFB955F1C9925 CRC64;
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O5JUL-2004 (TrEMBLrel. 2
 NUCLECTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.
Gao G., Vandenberghe L.H., Alvira M.
Wilson J.M.;
                                    Adeno-associated virus.
Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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                                                                                                                                                                                 EFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGL
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Best Local S
Matches 622
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J. Virol. 78:6381-6388(2004).
EMBL; AYS30622; AAS99307.1; -; Genomic_DNA.
SMR; Q6GBZ7; 217-735.
G0; GO:0019028; C:viral capsid; IEA.
G0; GO:0005199; F:structural molecule activity; IEA.
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 735 AA; 81947 MW; EBA318E904E0BF0A CRC64;
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                                                                                                                      GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGV
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                                                         YSEPRPIGTRYLTRNL
                                                                  YTEPRPIGTRYLTRPL
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                                                                                                EFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGL
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                   PRELIMINARY;
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Pred. No. 3.5e
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Matches 634
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EMBL; AYS30567; AAS99252:1; -; Genomic_DNA.

SNR; Q6GC52; 218-737.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat; 1.

SEQUENCE 737 AA; 81538 MW; CC68EB97BE11F25C
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
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Viruses; ssDNA viruses;
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  PPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDN
                                                                                  NQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQILIKNTPVPAN
                                                                                                                                                                                     GVLIFGK--TGATNKTTLENVLMTNEEEIRPTNPVATEEYGIVSSNLQAANTAAQTQVVN
                                                                                                                                                                                                                                                                                        LPGPCFRQQRVSKTLDQNNNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDEDRFFPSS
                                                                                                                                                                                                                                                                                                                      LPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMS
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85.8%; Pred. No. 3.56
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Wilson J.
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LPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMS
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SMR; Q6JC58; 218-737.
GO; GO:0019028; C:viral capsid; IEGO; GO:0005198; F:structural molec InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 737 AA; 81486 MW; EF6
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QGJC58;
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05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
Capsid protein VP1.
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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EMBL; AY530561; AAS99246.1; -;
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                     PFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQ-NQSGSAQNKDLLFSRGSPAGMSVQPKNW
                                                                                             QGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEV
                                                                                                                                                LINSNWGFRPKKLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAH
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PFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNAGGTAGNRELQFYQGGPTTMAEQAKNW
                                                                      QGCLPPFPADVFMIPQYGYLTLNNGSQSVGRSSFYCLEYFPSQMLRTGNNFTFS
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85.6%; Pred. No. 4.1e-215;
tive 48; Mismatches 55;
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J. Virol. 78:6381-6388(2004).
EMBL; AY550591; AAS99276.1; -;
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SEQUENCE 735 AA; 81897 MW; 197066F8911FAE9B CRC64;
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Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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GO:0019028; C:viral capsid; IEA.
GO:005198; F:structural molecule activity;
erPro; IPR001403; Parvo_coat.
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INNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
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                                                            TTSTRTWALPTYNWHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
                                                                                                    SVPDPQPLGQPPAAPSGLGSTTMATGSGAPMADNNEGADGVGNSSGNWHCDSQWLGDRVI
                                                                                                                  SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI
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RA Q6JCD-1
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U5-JUL-2004 (TrEMBLrel. 2:

O5-JUL-2004 (TrEMBLrel. 27

Capsid protein VP1.

Name=cap;
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QGJC19;
05-JUL-2004 (TrEMBLrel. 2)
05-JUL-2004 (TrEMBLrel. 2)
                                                                                                                                                                                                                 SMR; OGJC19; 218-738.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecul
GO; GO:0005198; F:structural molecul
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 738 AA; 81582 MW; 585F.
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EMBL; AY530600; AAS99285.1; -;
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NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
                                                                                                                                                                                                                                                                                                                                                                                                                                    Adeno-associated virus.
Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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Last sequence up
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8; Mismatches 61;
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                                                              VPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNW
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                                PTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDFAVNTE
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Search completed: November 23, 2005, 17:41:16 Job time: 144.766 secs

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Maximum Match 10
Listing first 45
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Copyright (c) 1993 - 2005 Compugen Ltd.
  2005, 17:29:19; Search time 25.9904 Seconds (without alignments)
2724.684 Million cell updates/sec
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C;Species: adeno-associated virus type 2
C;Species: o5-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004
C;Accession: A03698
R;Srivastava, A.; Lusby, E.W.; Berns, K.I.
Uirol. 45, 555-564, 1983
A;Title: Nucleotide sequence and organization of the adeno-associated virus 2 genome.
A;Reference number: A03694; MUID:83164299; PMID:6300419
A;Accession: A03698
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-504 <SRI>A;Residues: 1-504 <SRI
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Length 504;

nuclear pore prote	A35622	_	1076	2.9	117.5	ຫ
myrosinase-binding	T08144	N	956	3.0	118	4
probable transketo	T52289	N	739	3.0	118	ω
toxin-like outer m	H71879	N	2399	3.0	118.5	N
transcription tact	A41311	N	667	3.0	119	_
probable membrane	AC0314	2	2004	3.0	119.5	0
IgA-specific serin	S60762	N	1394	3. 0	119.5	9
hypothetical prote	E86719	N	1180	3.0	119.5	æ
hypothetical serin	T37752	N	1379	3.0	120	7
type VII collagen	I48103	N	1549	3.0	121	σ
$\boldsymbol{\pi}$	S28925	N	1113	3.0	121	u
protein F2K11.10 (F96660	N	635	3.O	121	4
valine-tRNA ligase	SYBSVS	سر	880	3.1	122.5	ω
enamelin precursor	T37455	N	1142	3.1	123	N
toxin-like outer m	B64635	N	2529	3.1	123.5	_
probable TonB-depe	AB0124	N	690	3.1	123.5	0

ALIGNMENTS

392; 623 503 120 300 240 443 180 383 NGSQAVGRSSFYCLEYFBSQMLRTGNNFTFSYTFEEVFFHSSYAHSQSLDRLMNPLIDQY PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPABFSATKFASFITQYSTG BBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI WTGATKYHLNGRDSLVNP--AMASHKDDEEKFFPQSGVLIFGKQGSEKTNVNIEKVMITD WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD LYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYS LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQY EEEIGTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKI Conservative 54.6%; Score 2177.5; DB 1; 82.5%; Pred. No. 3.9e-134; ive 33; Mismatches 47; Indels ω --Gaps 382 622 562 502 442 179 119 322 60 357 299 239

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coat protein VP1 - muscovy duck parvovirus

//Alternate names: VP1 protein

C;Species: muscovy duck parvovirus
C;Date: 19-Max-1997 #sequence_revision 19-Max-1997 #text_change 09-Ju1-2004
C;Accession: S52210

R;Zadori, Z.; Erdei, J.; Nagy, J.; Kisari, J.
submitted to the EMBL Data Library, September 1993
A;Reference number: S52209
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A;Molecule type: DNA
A;Residues: 1-732 <ZAD>
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LKNPPPQILIKNTPVPANPPABFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEV
                                                                                                                                                                                                                                                                                                         LRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLF
                                                           TVTNEQNTTTAPTNAELEVLGALPGMVWQNRDIYLQGPIWAKIPKTDGKPHPSPNLGGFG
                                                                                                                                 PVATTHIEDQASSVPAQNIIGIAKDPYRSGSTLAGISDIMVTDEQEIAPTNGVGWRPYGL
                                                                                                                                                                    TAMASHKDDEDKFFPMSGVMIFGKE--SAGASNTALDNVMITDEEEIKATNPVATERFGT
                                                                                                                                                                                                                                            SRGSPAGMSVQPKNWLPGPCYRQQRVSKTK--TDNNNSNFTWTGASKYNLNGRESIINPG
                                                                                                                                                                                                                                                                                                                                                           NEHQLPYVLGSATEGTMPPFPSDVYALPQYGYCTMHTNQSGARFNDRSAFYCLEYFPSQM
                                                                                                                                                                                                                                                                                                                                                                                          SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN---NGSQAVGRSSFYCLEYFPSQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTTUDGVTTIANNLTSTVQVFSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLDKGPPVNKADSVALEHDKAYDQQLKAGDNPY1KFKHADQEF1DNLQGDTSFGGNLGKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWLEDNLSEGIREWWDLKPGAPKPKANQQKQ------DDGRGLVLPGYKYLGPFN
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                                                                                             VAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ENSPSPSNSGGEASAAATEGSEPVAAP-----NMAEGGSGAMGDSAGGADGVGNASG
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                                                                                                                                                                                                            KKAVKGAFGAMGRNWLPGPKLLDQRVRAYSGGTDNYANWS1WSKGNKVFLKDREYLLQPG
                                                                                                                                                                                                                                                                                   LRTGNNFEFSFEFEEVPFHSMFAHSQDLDRLMNPLLDQYLWNFSEV-NGGRNAQ-----F
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Pred. No. 2.6e-133;
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A;Title: Complete nucleotide sequence and genome organization A;Reference number: A26104; MUID:87061184; PMID:3783814
A;Reference DNA
A;Residues: 1-673 < CHE>
A;Residues: 1-673 < CHE>
C;Superfamily: parvovirus coat protein
C;Keywords: Coat protein
C;Keywords: Coat protein VP2 #status predicted < VP2>
F;138-673/Product: coat protein VP2 #status predicted < VP2>
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N;Contains: coat protein VP2

C;Species: bovine parvovirus

C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Ju1-2004

C;Accession: A26104
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNP
       TFTREARTKLITGSNGADGDYKEWWMLPNOMWDSAPISRYNPIWVKVPRVNRKTLLDTOD
                                          REGIVAVNEQSSSIDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHIDGHEHPSPLM
                                                                                                                    M-----IFGKE----
                                                                                                                                                                                         GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGV
                                                                                                                                                                                                                                                               NPLIDQYLYYLNRTQN-----QSGSAQNKDLLFSRGSP-----AGMSVQPKNWLP 480
                                                                                                                                                                                                                                                                                                                                                                              GAMGTVYNNDLTAGMHIFCDGDHRYPYVQHPWDDQCMPELPNSIWELPQYAYIPAPISVV
                                                                                                                                                                                                                                                                                                                                                                                                             DGVTTIANN-LISTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEP--PATPAAVGPTTMASGG
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                                                                              RAVRVGYSTDPIYGGQQPESDLLRLRYSASAAEGQQNPILEN
                                                                                                                                                                                                                           RIYIQLWRLRMDRKQHHIQHASDDVQSTGQKQKNLLIQRTKQPNKQRFQNAALRTSNWMS
                                                                                                                                                                                                                                                                                                    DNNTTNTVEEHLLKGVPLYMLENSDHEVLRNG-----
                                                                                                                                                                                                                                                                                                                                          -NNGSQAVGRS-----SFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLM 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------RGGSGVGYSTGGWTGGTIFSENIVVTKNTRQFICDIKNGHLYKS-EVLNTGD
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28.6%; Pred. No. 3.7e-44;
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                                                                                                                  -----SAGASNTALDNVMITDEEEIKATNPVATE
                                                                                                                                                      GIARGTHNATLQTQSAGALVTMVTNGAD----VSGV
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A;Cross-references: UNIPROT:P07299; UNIPARC:UPI0000127D7C; C;Superfamily: parvovirus coat protein C;Keywords: coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Nucleotide sequence and genome organization of A;Reference number: A24299; MUID:86200451; PMID:3701931 A;Accession: A24299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coat protein VP1 - parvovirus B19 (strain Au)
C;Species: parvovirus B19
A;Note: host Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Ju1-2004
C;Accession: A2429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
VCPV19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-781 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Shade, R.O.; Blundell, M.C.; Cotmore, S.F.; Tattersall, J. Virol. 58, 921-936, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            577
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| | | : | : | : | : | : | : |
| wrpeymis---atimsvdaytinnagvy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISSASTGASND-----NHYFGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSIPMSHPPGTIFIKLARIPVPGNGD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGFGLKNPPPQILIK--NTPVPANPPABFSATKFASFITQYSTGQVSVEIBWELQKENSK
                                                                                                                                                                                                                                                                                                                                                                                                                              NNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNN-GSQAVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVT--TNDGVTTIA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MWSEGATFSANSVTCTFSROFLIPYDPEHHYKVFSPAASSCHNASGKEAKVCTISPINGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPGTNYVGPGNELQAGPPQSAVDSAARIHDFRYSQLAKLGINPYTHWTVADEELLKNIKN
PIWAKIPHTDGHFHPS-PLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYS
                                                                                                                                                                  GASKYNLNGRESIINPG-TAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNV-----
                                                                                                                                                                                                                                                     YLNRTONOSGSAONKDLLFSRGSPAGMSVOPKNWLPGPCYROORVSKTKTDNNNSNFTWT
                                                                                                                                                                                                                                                                                                  KLASEESAFYVLEHSSFQLLGTGGTASMSYKFPPVPPENLEGCSQHFYEMYNPL---YGS
                                                                                                                                                                                                                                                                                                                                                                                    DSTTGRLCMLVDHEYKYPYVLGQGQDTLAPELPIWVYFPPQYAYLTVGDVNTQGISGDSK 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STPWRYLDFNALNLFFSPLEFOHLIENYGSIAPDALTVTISEIAVKDVTDKTGGGV-QVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYNA----SEKYPSMTSVNSAEASTGA-----GGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKKRLNFGQTGDSESVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETGFQAQVVKDYF----
                                                                                                                         GLSTGTSQNTRISLRPGPVSQPYHHWDTDKYVTGINAISHGQTTYG---NAEDKEYQQGV
                                                                                                                                                                                                                 RLGVPDTLGGDPKFRSL-----THEDHAIQPQNFMPGPLVNSVSTKEGDSSNTGAGKALT
                                                                                                                                                                                                                                                                                                                                           ----RSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQYLY
                                                                                 --MITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.1%; Score 600.5; DB 1; 26.6%; Pred. No. 3.5e-31;
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                                        --FPNKGTQQYTDQIE-RPLMVGSVWNRRALHYES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
A60006
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C;Keywords: coat protein; glycoprotein
F;151-729/Product: coat protein VP2 #Btatus predicted <VP2>
F;172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Sakurai, M.; Nishimori, T.; Ushimi, C.; Nakajima, Virus Res. 13, 79-86, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-729 <SAK>
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coat protein VP1 - porcine parvovirus (strain N_1Contains: coat protein VP2
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                676 TGQVSVEIEWEL-QKENSKRWNPE
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    580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 RGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQE
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                                             QYNDDE----PNGAIRFTMGYQHGQLTTS-----SQELERYTFNPQSKCGRAPKQQFNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVAGQMVQDDAHTQMVTPWSLIDANAWGVWFNPADWQLISNNMTEINLVSFEQEIFNVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNNEGADGVGNASGNWH--CDSTWLGD---RVITTSTRTWALPTYNNHLYKQIS--SAST
                                                                                       SHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITDEEEIKATNP-----VATERFGT
                                                                                                                                                                           PAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINP--GTAMA
                                                                                                                                                                                                                                                            EVPFHSSYAHSQSLDR------LMNPLI--DQYLYYLNRTQNQSGSAQNKDLLFSRGS
                                                                                                                                                                                                                                                                                                     YLSCTRNLNPPTYTGQSQQITDSIQTGLHSDIMFYTIENAVPIHLLRTGDEFSTGIYHFD
                                                                                                                                                                                                                                                                                                                                                    L-----TLNNGSQAVGRS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPRHIFINLAKKKAKGTSNTNSNSMSENVEQHNPINAGTEL-SATGNESGGGGGGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAAVGPTTMASGGGAPMA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETEHAKDYGGKIGHYFFRA-KRAFRP--KLSETDSPTTSQQPEVRRSPRKHPGSKPPGKR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGLTLPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYDKYIKSGKNPYFYFSAADEKFIK 68
                                                                                                                                                                                                                   TKPL--KLTHSWQTNRSLGLPPKLLTEPTTEGDQHPGTLPAANTRKGYHQTMNNSYTEAT
                                                                                                                                                                                                                                                                                                                                                                                             KTITESATSPPTKIYNNDLTASLMVALDTNNTLPYTPAAPRSETLGFYPWLPTKPTQYRY
                                                                                                                                                                                                                                                                                                                                                                                                                                     KEVT----TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAS----NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GGRGAGGVGVSTGSFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKRIHVLNSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.1%; Score 482; DB 1; Length 729; ilarity 25.7%; Pred. No. 1.7e-23; Conservative 112; Mismatches 314; Indels 1.
                                                                                                                                -----AQVGYNTPYMNFEYSNGGPF-----LTPIVPTADT
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PMID:2750278
                                                                                                                                                                                                                                                                                                                                                    --SFYCLE-YFPSQMLRTGNNF-TFSYTFE 417
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usat protein VPI - porcine parvovirus (strain NADL-2)

N;Contains: coat protein VP2

C;Species: porcine parvovirus

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C;Accession: B33743; D48472

R;Vasudevacharya, J: Basak, S.; Srinivas, R.V.; Compans, R.W.

Virology 173, 368-377, 1989

A;Title: Nucleotide sequence analysis of the capsid genes and the right-hand A;Reference number: A33743; MUID:90085785; PMID:2596019

A;Accession: B33743

A;Molecula **----
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C;Keywords: coat protein; glycoprotein
F;151-729/Product: coat protein VP2 #status predicted
F;32,172,198,282,330,433,471,573,604,651/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 11-729 <BER>
A;Cross-references: UNIPARC:UPI0000174965
A;Experimental source: NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Bergeron, J.; Menezee, J.; Tijssen, P.
Virology 197, 86-98, 1993
A;Title: Genomic organization and mapping of transcription and
A;Reference number: A48472; MUID:94025614; PMID:8212598
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C; Superfamily: |
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A; Residues: 1-729 < VAS>
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                                                                                                        GVAGQMVQDDAHTQMVTPWSLIDANAWGVWFNPADWQLISNNMTEINLVSFEQEIFNVVL
                                                                                                                                                                                                                                                     PAPRHIFINLAKKKAKGTSNTNSNSMSENVEQHNPINAGTEL-SATGNESGGGGGGG---
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                                                                                                                                            GAS----NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQV
                                                                                                                                                                               -GGRGAGGVGVSTGTFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKRIHVLNSES
                                                                                                                                                                                                                 DNNEGADGVGNASG--NWHCDSTWLGD---RVITTSTRTWALPTYNNHLYKQIS--SAST
                                                                                                                                                                                                                                                                                      -----TGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAAVGPTTMASGGGAPMA
                                 KTITESATSPPTKIYNNDLTASLMVALDTNNTLPYTPAAPRSETLGFYPWLPTKPTQYRY
                                                                     KEVT----TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGY
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-TLNNGSQAVGRS-----SFYCLE-YFPSQMLRTGNNF-TFSYTFE
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                                                                                                                                                         KIPHTD--GHFHPSPLMGGFGLK-NPPPQILIKNTPVPANPPAEFSA-TKFASFITQYST
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                                                                                                                                                                                                                                                              ERFGTVA-VNFQSSS-----TDPATG--DVHAMGALP-----GMVWQDRDVYLQGPIWA 620
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FWWKGTLTFTAKMRSSNMWNPIQQHTT---
                                                    GQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                        KELDTÖLKPRLH---VTAPFVCKNNPPGÖLFVKIAP---NLTDDFNADSPQQPRIITYSN
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Ricarlson, J.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Winston, S.; Hahn, W.
J. Virol. 55, 574-587, 1985
A; Title: Cloning and sequence of DNA encoding structural proteins of the autonomous parve A; Reference number: A03697; MUID:85265017; PMID:2991581
A; Accession: A03701
A; Accession: A03701
A; Molecule type: DNA
A; Residues: 1-727 < CAR>
A; Cross-references: UNIPROT:P04864; UNIPARC:UPI0000127D55; EMBL:M10824; NID:g333474; PID: C; Genetics: A; Introns: 11/1
C; Genetics: Coat protein
C; Keywords: coat protein
C; Keywords: coat protein VP2 #status predicted < VP2> N;Contains: coat protein VP2
c;Species: feline panleukopenia virus,
C;Date: 30-Jun-1987 #sequence_revision
C;Accession: A03701
R;Carlson, J.; Rushlow, K.; Maxwell, I. coat protein VP1 - feline panleukopenia virus Query Match Best Local Local Similarity 163 103 RLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKT 162 187; 10 43 GQQPAKKRLNFGQTGDSESVP----DPQPLGEPPA--TPAAVGPTTMASGGGAPMADNNE 216 RGLVLPGYKYLGPFNGLDKGEPVNAADAAALBHDKAYDQQLKAGDNPYLRYNHADAEFQE 102 ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 322 GADGVGNASGNWH-----CDSTWLGDRVITTSTRTWALPTYNNHLYKQI-----SS 262 QTKDATDWGGKIGHYFFRAKKAIAPVLTDTPDHPSTSRPTK-PTKRSKPPPHIFINLAK- 127 -----KKKAGAGQVKRDNQAPMSDGAVQPDGGQPAVRNERATGSGNGSGGGG------GG 176 RGLVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYAAYLRSGKNPYLYFSPADQRFID Conservative 117; Mismatches 11.1%; Score 444.5; 23.7%; Pred. No. 4.6 Pred. No. 4.6e-21; FPLV 30-Jun-1987 #text_change 09-Jul-2004 -EITANSSRLVHLNMPESENYKRVVVNNMDKTA DB 1; Length Indels 189; 727; Gaps 234 69

VKGNMALDDTHVQIVTPWSLVDANAWGVWFNPGDWQLIVNTMSELHLVSFEQEIFNVVLK

294

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A; Molecule type: DNA
A; Residues: 1-722 «KAR»
A; Cross - references: UNIP)
C; Superfamily: parvovirue
C; Keywords: coat protein
F; 139-722/Product: coat )
                                                                                                                                                                                                                                                                                                                                                          coat protein VPI - mink enteritis virus (strain Abashiri)
N;Contains: coat protein VP2
C;Species: mink enteritis virus, MEV
C;Species: mink enteritis virus, MEV
C;Accession: B3850
C;Accession: B3850
R;Kariatsumari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishigurio, N.; Goto, H.;
J. Gen. Virol. 72, 867-875, 1991
A;Title: Construction and nucleotide sequence analysis of an infectious DNA clone A;Reference number: A38350; MUID:91202123; PMID:2016597
A;Accession: B38350
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;Keywords: coat protein
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Best Local
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                                                                                                                                                                   GLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQER 103
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                                                                                         TKDATDWGGKIGHYFFRAKKAIAPVLTDTPDNPSTSRPTK-PTKRSKPPPHIFINLAK--
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 ADGVGNASGNWH - - -
                                                          QQPAKKRLNFGQTGDSESVP----DPQPLGEPPA--TPAAVGPTTMASGGGAPMADNNEG 217
                                                                                                                  LQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTG 163
                                                                                                                                                 GLVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYAAYLRSGKNPYLYFSPADQRFIDQ
                            ----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERATGSGNGSGGGG-----GGG
                                                                                                                                                                                                           11.0%; Score 439.5; DB 1; llarity 23.6%; Pred. No. 9.6e-21; Conservative 117; Mismatches 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          728
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                                                                                                                                                                                                                                                                       protein VP2 #status predicted
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   -CDSTWLGDRVITTSTRTWALPTYNNHLYKQI - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GKTGINY--TNIFNTYGPLTALNNVP------PVYPNG
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                                                                                                                                                                                                                                                                          <VP2>
                                                                                                                                                                                                               Indels 189;
                                                                                                                                                                                                                                         Length
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A;Molecule type: DNA
A;Residues: 1-727 <MAR>
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STGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKE
                                                                                                                                                                                                                          ANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN---
                                                                                                                                                                                                                                                                                                                                                                                                                                 LPVTNDNVLLPTDPIG----GKTGINY--TNIFNTYGPLTALNNVP-----PVYPNGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASKY---NLNGRESIINPGT----AMASHKDDEDKFFPMSGVMIFGKESAGASNTALD-N
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                                                                                                                                                                                                                                                                                                                                                                              IWAKIPHTDGHFHPSPLMGGFGLK------NPPPQILIKNTPVPAN---PPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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(strain
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coat protein VP1 - feline panleukopenia virus (stra N;Contains: coat protein VP2 C;Species: feline panleukopenia virus, FPLV C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 C;Accession: B36608 C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;144-727/Product: coat protein VP2 #status predicted R;Martyn, J.C.; Davidson, B.E.; Studdert, M.J.
J. Gen. Virol. 71, 2747-2753, 1990
A;Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine A;Reference number: A36608; MUID:91073139; PMID:2174965 A;Cross-references: UNIPROT: P24840; UNIPARC: UPI0000127D56; 103 RLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKT : |: | : | | :: | : | : | : | h 10.8%; Similarity 23.5%; RGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQE 102 RGLVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYAAYLRSGKNPYLYFSPADQRFID Conservative 117; Mismatches Score 431.5; DB 1; Pred. No. 3.2e-20; Pred. No. 3.2e-20; #text_change 09-Jul-2004 Indels Length GB:X55115 189; Gaps 162 69

parv

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RESULT 10
VCPVPP
VCPVPP
Coat protein VP1 - porcine parvovirus
N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Accession: B33302
C;Accession: B33302
C;Accession: B3302
C;Accession: B3302
A;Renz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A;Title: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971
A;Accession: B33302
A,MCleonia type. NA
                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-723 < RAN>
A; Cross-references: UNI
C; Genetics:
                                                                                                            C;Genetics:
A;Introns: 10/1
                                         ;145-723/Product:
                                                                ;Superfamily: pa
;Keywords: coat
Query Match
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                                                                                  parvovirus coat protein
                                                                protein
                                         coat protein VP2 #status predicted <VP2>
                                                                                                                                                        UNIPROT: P18546; UNIPARC: UPI0000174964; EMBL: D00623
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  10.7%;
  Score
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Length 723;
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                                                                             621
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TAKMRSSNMWNPIQQHTT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNASGNWH--CDSTWLGD---RVITTSTRTWALPTYNNHLYKQI-----SSASTGAS-ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOOPAKKRINFGOTGDSESVPDPOPLGEPPATP-AAVGPTTMASGGGAPMADNNEGADGV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIGHYFFRAKRAFAPKL---SETDSPTTSQQPEVRRSPRKHPGSKPPGKRPAPRHIFINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGPGNSLDQGEPTNPSDAAAKEHDEAYDKYIKSGKNPTFYFSAADEKFIKETEHAKDYGG
                                                                                                                                                                                                                                       FPMSGVMIFGKESAGASNTALD---NVMITDEEEIK--ATNP-----VATERFGTVA-V
                                                                                                                                                                                                                                                                                                                                                                                                            PPTYTGQSQPNNRLNTNRLHSDIMFYTIENAVPIHLLRTGDEFSTGIYHFDTKPL--KLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPTKIYNNDLTASLMVALDTNNTLPYTPAAPRSETLGFYPWLPTKPTQYRYYLSCIRNLN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKKKAKGTSNTNSNSMSENVEQHNPIN--AATELSATGNESGGGGGG----GGRGAGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGPFNGLDKGEFVNAADAAALEHDKAYDQQLKAGDNFYLRYNHADAEFQERLQEDTSFGG
                                            ELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                             RLH---VTAPFVCKNNPPGQLFVKIAP---NLTDDFNADSPQQPRIITYSNFWWKGTLTF
                                                                                                          HFHPSPLMGGFGLK-NPPPQILIXNTPVPANPPAEFSA-TKFASFITQYSTGQVSVBIEW
                                                                                                                                              NLENTINGTLLPSDPIGGKSNMHFMNTLNTYGPLTALNNTAPVFPNGQIWDKELDTDLKP
                                                                                                                                                                         NFQSSS-----TDPATG--DVHAMGALP-----GMVWQDRDVYLQGPIWAKIPHTD--G
                                                                                                                                                                                                                                                                                                            NWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINP--GTAMASHKDDEDKF
                                                                                                                                                                                                                                                                                                                                           HSWQTNRSLGLPPKLLTEPTTEGDQHPGTLPAANTRKGYHQTINNSYTEAT----AIRP-
                                                                                                                                                                                                                                                                                                                                                                                                                               --TLNNGSQAVGRSS-----FYCLE-YFPSQMLRTGNNF-TFSYTFEEVPFHSSYA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYL-----
                                                                                                                                                                                                                                                                                                                                                                             HSQSLDR-----LMNPLI--DQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPK 476
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                                                                                                                                                                                                            --GAIRFTMDYQHGHLTTSSQELERYTFNPQSKCGRAPKQQFNQQAPL
                                                                                                                                                                                                                                                                           AQVGYNTPYMNFEYSNGGPF-----LTPIVPTADTQYNDDEPN-
             TAENIGKYI-PTNÍG
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A;Accession: B23008
A;Molecule type: DNA
A;Residues: 1-718 <SAH>
A;Cross-references: UNIPROT:P07302; UNIPARC:UPI0000174963;
R;Astell, C.R.; Gardiner, E.M.; Tattersall, P.
J. Virol. 57, 655-669, 1986
                                                                                                                                                                                                                                                                                      coat protein VP1 - minute virus of mice (strain MVMi) c;Species: minute virus of mice, murine parvovirus C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #t. C;Accession: B23008; B29510
                                                                                                                                                                         R;Sahli, R.; McMaster, G.K.; Hirt, B.
Nucleic Acids Res. 13, 3617-3633, 1985
A;Title: DNA sequence comparison between two tissue-specific A;Reference number: A23008; MUID:85242059; PMID:3855242
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                                                                NID: 960918;
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A;Title:

DNA sequence of the lymphotropic variant of minute virus of

mice, MVM(i),

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PIDN

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A;Reference number: A29510; MUID:86115415; A;Accession: B29510
A;Molecule type: DNA
A;Residues: 1-143; A; 145-718 <AST>
A;Cross-references: UNIPARC:UPI0000127D6C; C;Superfamily: parvovirus coat protein C;Keywords: coat protein
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coat protein VP1 - canine parvovirus (strain N;Contains: coat protein VP2 C;Species: canine parvovirus, CPV C;Date: 30-Jun-1989 #sequence_revision 30-Jun C;Accession: B29962 R;Reed, A.P.; Jones, E.V.; Miller, T.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYDQYIKSGKNPYLYFSAADQRFIDQT
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                                                                                                                                                                                                                                                                                                                                                                                       RGSPAGMSVQPKNWL-----
                                                                                                                                                                                                                                                                                                                                                                                                                   DEFATGTYYFDTNPV--KLTHTWQTNRQLGQPPLLSTF----PEADTDAGT-----LTA
                                                                                                                                                                                                                                                                                                                                                                                                                                            NNF-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQSGSAQNKDLLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADVFMIPQYGY------LTLNN------GSQAVGRSSFYCLEYFPS-QMLRTG
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                                                                                                                                        SRIVTYGTFFWKGKLTMRAKLRA----NTTWNPVYQ----
                                                                                                                                                                                           SPVYPQGQIWDKELDLEHKPRLHITAPFV---CKNNAPGQMLVRLGPNLTDQYDPNGATL
                                                                                                                                                                                                                       RDVYLQGPIWAK---IPHTDGHFHPSPLMGGFGLKNPPPQILIKNTP--VPANPPAEFSA
                                                                                                                                                                                                                                                                          NTALDNVMITDEEEIKATNPVATERFGTVAVNFQS--SSTDPATGDVHAMGALPGMVWQD
                                                                                                                                                                                                                                                                                                        ANGSVRYSYGKOHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIOSAPLVVPPPLNGIL
                                                                                                                                                                                                                                                                                                                                  FTWTGASKYNLNGRESIINPGTAMASHKDDEDKF-----FPMSGVMIFGKESAGAS
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                                                                                                                                                                TKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNG 719
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                                                                                                                                                                                                                                                   ----NPIGTKN----DIHFSNVFNSYGPLTAFSH------P
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J. Virol. 62, 266-276, 1988
A;Title: Nucleotide sequence and genome organization of canine A;Reference number: A29962; MUID:88062992; PMID:2824850
A;Accession: B29962
A;Accession: B29962
A;Molecule type: DNA
A;Residues: 1-748 <REE>
A;Cross-references: UNIPROT:P12930; UNIPARC:UPI0000127D7B; EMBL
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 26/3
C;Superfamily: parvovirus
C;Keywords: coat protein
F;165-748/Product: coat pr
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Best Local Similarity 23.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 GLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADGVGNASGNWH-----CDSTWLGDRVITTSTRTWALPTYNNHLYKQI-----SSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQPAKKRLNFGQTGDSESVP----DPQPLGEPPA--TPAAVGPTTMASGGGAPMADNNEG
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                                                                              TPVPAN----PPAEFSATKFASFITQYSTGQVSVEIEWELQKEN9KRWNPEVQYTSNYAKS
                                                                                                                                                                                                              YPEGDWIQNINFNLPVTNDNVLLPTDPIG----GKTGINY--TNIFNTYGPLTALNNVP-
                                                                                                                                                                                                                                                                                                 PIAAGRGGAQTYENQAADGDPRY-----AFGRQHGQKTTTTGETPERFTYIAHQDTGR
                                                                                                                                                                                                                                                                                                                                             AMASHK-----
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                                                                                                                                                                      MVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK------
ANVDETVDNNGLYTEPRPIG
                                           APNLTNEYDPDASANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN----
                                                                                                                             ----PVYPNGQIWDKEFDTD
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Pred. No. 1.5e-19;
L4; Mismatches 287
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                                                                                                                               LKPRLHVNAPFVCQNNCPGQLFVKV
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VDNQFNYV-PSNIG

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coat protein VP1 - canine parvovirus (strain CPV-d)
%;Contains: coat protein VP2
C;Species: canine parvovirus, CPV
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990
C;Accession: A31163
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C;Keywords: coat p:
F;584-737/Product:
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A; Residues: 1-737 < PAR>
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Best Local
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                                                                                                                                                                                                                                                                                                                   SYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAG
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                                                                                                                                                                             ----GTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD-----
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                                                                                                                                                                                                                                                                                                                                                      YFQWDRTLIPSH-----TGTSGTPTNIYHGTDPDDVQFYTIENSVPVHLLRTGDBFATG
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                                  RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK------
                                                                    WIQNINFNLPYTNDNVLLPTDPIG----GKTGINY--TNIFNTYGPLTALNNVP-----
                                                                                                                                          KTPIAAGRGGAQTDENQAADGNPRYAFGRQHGQKTTTTGETPERFTYIAHQDTGRYPEGD
                                                                                                                                                                                                                                                                                    TFFFDCKP--CRLTHTWQTNRALGLPP-----FLNSLPQSEGATNFGDI------G
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 - PVYPNGQIWDKEFDTD-
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; PMID:3176341
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 LKPRLHVNAPFVCQNNCPGQLFVKVAPNLT
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ITDEEEIKA-TNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPI
                                    GKOHGEDWAKOGAAPERYTWDAIDSAAGRDTARCFV-----
                                                                       NGR--ESIINPGTA-------MASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVM
                                                                                                                                                                             LKLTHTWQTNRHLACLQGITDLFTSDTATASLTANGDRFGSTQTQNVNYVTEALRTRPAQ
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                                                                                                                                                                                                                                                                                                                       QGAGQDAIKVYNNDLTACMMVALDSNNILPYTPAAQTSETLGFYPWKPTAPAPYRYYFFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSLDQGEPTNPSDAAAKEHDEAYDQYIKSGKNPYLYFSPADQRFIDQTKDAKDWGGKVGH
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                                                                                                                                          -----SRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNL
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                                                                                                                                                                                                                                                                                    PQYGYLTLNNGSQ-----AVG-----RSSFYCLE-YFPSQMLRTGNNFTF-SYTFEEVP
                                                                                                                                                                                                                                                                                                                                                      ----NDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCL-----PPFPAD----VFMI 373
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--TSGVSRPGKRTKPPAHIFVNQ 112

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---- LDITAGEDHDAN----GAIRFNY

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290

231 267

-QSAPISIPPNQNQI

618 563

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C;Species: parvovirus H1
A;Note: host Homo sapiens (man)
A;Note: 14 -Nov-1983 #sequence_revision 14-Nov-1983 #text_ch
C;Date: 14 -Nov-1983 #sequence_revision 14-Nov-1983 #text_ch
C;Accession: A03699
R;Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nucleotide sequence of H-1 and A;Title: Parvovirus genome: nucleotide sequence of A;Reference number: A03695; MUID:83112183; PMID:6823009
A;Accession: A03699
                                                                                                     A;Molecule type: DNA
A;Residues: 1-722 <RHO>
A;Cross-references: UNIPROT:P03136; UNIPARC:UPI0000127D7D;
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEYDPDASANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN--
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                     Score 404; DB 1
Pred. No. 2e-18;
Mismatches
                                                 DB 1; Length 722;
290;
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Indels 178;
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. Virol. 54, 630-633, 1985 . Virol. 54, 630-633, 1985 . Pitel: Nuclectide sequence of the coat protein gene of canine parvovirus Reference number: A03702; MUID:85185696; PMID:3989914 . Recession: A03702 . MOlecule type: DNA . Residues: 1.722 < RIGO . Cross-references: UNIPROT:P04863; UNIPARC:UPI0000174966; EMBL:M10989 . Genetics: . Cross-references: UNIPROT:P04863; UNIPARC:UPI0000174966; EMBL:M10989 . Genetics: . Introns: 11/1 . Superfamily: parvovirus coat protein . Reywords: coat protein . Parvovirus predicted < VP2> . Parvovirus coat protein . Parvovirus coat protein . Parvovirus predicted < VP2> . Parvovirus coat protein . Parvovirus predicted < VP2> . Parvovirus coat protein . Parvovirus predicted < VP2> . Parvovirus coat protein . Parvovirus predicted < VP2> . Parvovirus predicted < VP2> . Parvovirus coat protein . Parvovirus predicted < VP2> . Parvovirus coat protein . Parvovirus predicted < VP2> . Pa	190 197 197 197 197 197 197 197 197 197 197
PROT: P04863; UNIPARC: UPI0000174966; EMBL:1 PROT: P04863; UNIPARC: UPI0000174966; EMBL:1 BE COAL Protein protein VP2 #status predicted <vp2> 9.7%; Score 385.5; DB 1; Length 72: 22.8%; Pred. NO. 3.1e-17; 7ative 118; Mismatches 297; Indels 1: - - - - - </vp2>	p1 - canine parvovirus (strain 780929) it protein VP2 line parvovirus, CPV 1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-200, 23702 20-633, 1985 ocide sequence of the coat protein gene of canine parvovirus mber: A03702; MUID:85185696; PMID:3989914 e: DNA 722 <rho #status="" 1="" <vp2="" coat="" embl:m10989="" nces:="" parvovirus="" predicted="" protein="" uniparc:upi0000174966;="" uniprot:p04863;="" vp2=""> 9.7%; Score 385.5; DB 1; Length 722; imilarity 22.8%; pred. No. 3.1e-17; imilarity 22.8%; pred. No. 3.1e-17;</rho>
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3, 1985 sequence of the coat protein gene of canine A03702; MUID:85185696; PMID:3989914 HO> UNIPROT:P04863; UNIPARC:UPI0000174966; EMBL: UNIPROT:P04863; UNIPARC:UPI0000174966; EMBL: UNIPROT:P04863; UNIPARC:UPI0000174966; EMBL: Virus coat protein tein oat protein VP2 #status predicted <vp2> 9.7%; Score 385.5; DB 1; Length 72: ity 22.8%; Pred. No. 3.1e-17; servative 118; Mismatches 297; Indels 1: pFNGLDKGEPVNAADAAALEHDKAYDQLKAGDNPYLRYNHADA </vp2>	ine parvovirus (strain in VP2 ovirus, CPV ovirus, CPV solvinus, CPV squence_revision 30-Jun 1985 quence of the coat prot 3702; MUID:85185696; PM 3702; MUID:85185696; PM 19701:01 protein in i
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ALIGNMENTS

Adeno-associated virus serotype 1; AAV-1; rep protein; cap protein; recombinant viral vector; gene delivery; 9 AAY71168 standard; protein; 599 AA 08-SEP-2000 AAY71168; 05-NOV-1998; 02-NOV-1999; WO200028061-A2. Adeno-associated virus 1. Adeno-associated virus serotype 1 capsid protein 18-MAY-2000. (UYPE-) UNIV PENNSYLVANIA. transgene; VP2. (first entry) 98US-0107114P 99WO-US025694. ; capsid prote gene therapy; protein;

The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a

Claim 7; Page 93-95; 108pp; English.

Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.

N-PSDB; AAD00772, AAD00778. WPI; 2000-376571/32 Wilson JM,

Xiao W;

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Query Match
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Matches 599
                                                                                                                                                                         Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy;
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                    02-NOV-1999;
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QVSVEIEWELQKENSKRWNESVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in ABB80231-34 represent vpl proteins derived from various adeno-associated virus (AAV) serotypes. These sequences were used in the scope of the invention for comparison with the cap protein derived from AAV serotype 9. The AAV capsid comprises three proteins vpl, vp2 and vp3, which are alternative splice variants. The AAV or the nucleic acid molecule is useful for preparing a medicament for delivering a transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated adeno-associated virus (AAV) comprising an AAV9 useful for preparing a medicament for delivering a transgene
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05-JUN-2002; 2002US-0386132P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    736
                                                                                                                                                                               NIQVKEVTTUDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG
                                                                                                                                                                                                                                                                                                                                                                                      VGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAA
LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
                                                                                                                                                                                                                                                                                      KQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLF
                                                                                                                                                                                                                                                                                                                                                           VGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLY
                                                                          YLTLNIGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPPHSSYAHSQSLDRLMNP
                                                                                                                                                       NIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG
                                                                                                                                                                                                                                                         KQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLF
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Pred. No. 1.4e-253;
Mismatches 0;
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01-MAY-2002;
05-JUN-2002;
                                                                        The present sequence is the protein sequence of the vpl capsid protein of adeno associated virus serotype 1 (AAVI). The invention provides the nucleic acid and amino acid sequences of novel AAVB and fragments of these sequences. Each of these fragments may be used in a variety of vector systems and host cells. Among the desirable fragments are the cap proteins, including vpl, vp2, vp3 and hypervariable regions, the rep proteins, including vp1, vp2, vp3 and hypervariable regions, the rep proteins, including rep78, rep68, rep52 and rep40, and the sequences encoding these proteins. The fragments may be used alone, in combination with other AAVB sequences or in combination with elements from other AAV or non-AAV viral sequences in the production of recombinant AAV and for use as antisense delivery vectors, gene therapy vectors or vaccine
                                                                                                                                                                                                                                                                                            New adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence of AAV8, useful for preparing a medicament for delivery of a transgene to a cell and for treating cystic fibrosis or hemophilia B.
                                                                                                                                                                                                                                                                                                                                                                                         Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adeno associated virus 1 capsid protein vpl
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                                                                                                                                                                                                                                                                 Disclosure; Fig 2A-C; 82pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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                                                from a
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                                                   claimed molecule comprises a cap protein of a functional rom a serotype selected from AAV1, AAV2, AAV3, AAV4, AAV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0341151P
2002US-0377133P
2002US-0386122P
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                                                serotype selected from AAV1, AAV2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus.
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13-NOV-2001;
17-DEC-2001;
01-MAY-2002;
                                                                                                                                                                                                                                                       adeno-associated virus; AAV; cytostatic; antipsoriatic; antirheumatic; antiarthritic; neuroprotective; antidiabetic; antithyroid; dermatological; antiinflammatory; gene therapy; vaccine; hyperproliferative; cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
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                                                               IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPARFSATKFASFITQYSTG
                                                                                                                                              VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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    QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
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Pred. No. 1.4e-253;
Mismatches 0;
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Length Indels

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Gaps

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360 437 300 377

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The invention relates to a novel method for detecting adeno-associated covirus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antipsoriatic, antirheumatic, antiarthritic, neuroprotective, antipsoriatic, antirhyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other aucoimmune diseases clike rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroidatis, scleroderma or Crohn's disease. This sequence represents an conditions sclerosian sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting adeno-associated virus sequences in a sample, usef preventing or treating hyperproliferative or autoimmune discomprises subjecting a sample having a DNA to amplification polymerase chain reaction.
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CC virion. Also described are: a polynucleotide encoding the mutated protein composition. Also described are: a polynucleotide encoding the mutated protein and cell vering a recombinant AAV virion to a cell or tissue of a vertebrate combinate. AAV virion is useful for delivering a delivering a recombinant AAV virion is useful for delivering a cell contissue of a vertebrate consider, where the protein encoded by the heterologous nucleic acid consecule is expressed at a level that provides a therapeutic effect, consecule is expressed at a level that provides a therapeutic effect, consecule is expressed at a level that provides a therapeutic primate mammalian consecutivity of primate consumers activity of primate consecutivity of primate consecutivity of primate industries decreased consecutivity of primate consecutivity of disorders such as the mophilia, plenylketonuria, Crigler-Najjar disease, Gout and Lesch-consecutivity of primate consecutive heart failure, cancer, inflammatory and immune disorders, muscular dystrophies, and consecutive consecutive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-2003; 2003US-0480395P.
30-APR-2004; 2004US-0567310P.
03-JUN-2004; 2004US-0576501P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; gene therapy; immunogenicity; virus inact; hemophilia; Pepck deficiency; galactosemia; phenylketonuria; Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia; atheroselerosis; thrombosis; embolism; Parkinson's disease; congestive heart failure; cancer; inflammation; immune disor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADV70294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mutated adeno-associated virus (AAV) capsid protein that when present in an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding wild-type virion, useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-2004; 2004WO-US019884.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a mutated adeno-associated virus (AAV) capsid protein that when present in an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding wild-type virion. Also described are: a polynucleotide encoding the mutated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5;
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                                              capsid protein
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Best Local Similarity
Matches 599; Conserv
                                                                                                                                                                                                                                                                                                  bacterial infection; cancer; ulcerative colitie; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; anti-HIV; antipsoriatic; vasotropic; gastrointestinal-gen; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADZ27069 standard;
  30-SEP-2003; 2003US-0508226P.
29-APR-2004; 2004US-0566546P.
                                                                                                                                                                                                                                                                                                                                                                                                           scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                       rheumatoid arthritis; multiple sclerosis; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adeno-associated virus protein
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                                                                                 2004WO-US028817
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Pred. No. 1.4e-253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
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Crohn's disease; hemophilia;
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Query Match
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Matches 599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adeno-associated virus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New adeno-associated virus (AAV) c
members, useful for preventing and
sclerosis, diabetes, scleroderma,
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                                                                                                                     IWAKI PHTDGHFHPS PLMGGFGLKNPPPQI LI KNTPVPANPPAEFSATKFASFI TQYSTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNP
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QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
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                                                                                            IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
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and/or treating arthritis, multiple
ma, psoriasis, hemophilia, HIV, bacterial
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an adeno-associated virus (AAV) clade comprise at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heurise by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, arcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiarthritic; neuroprotective; antiinflammatory; antidiabetic;
antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
virucide; antibacterial; cytostatic; antiulcer; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; bacterial infection; cancer; ulcerative colitis; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
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29-APR-2004;
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                                                                                                   KQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLF
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NIQVKEVTTNDGVTTI ANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPPPADVFMI PQYG
                                                                                                                                                                                 VGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLY
                                                           KQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLF
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ilarity 100.0%;
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The specification describes a method for lowering total cholesterol levels in a subject. The method comprises delivering to the subject a recombinant adeno-associated virus (AAV) comprising a gene encoding a human apolipoprotein E (apoE) or apoA under the control of a regulatory control sequence which directs expression of the gene. The recombinant AAV also comprises a capsid protein selected from an AAV serotype (e.g. AAV7 or AAV8) which preferentially expresses high levels of transgene in live. A therapeutically effective amount of apoE or apoA expression is obtained upon delivery of low dose of AAV. The method of the invention is
                                                                                                                                                                                                                                                                                                                    Lowering total cholesterol levels and treating atherosclerosis in subject comprises delivering a recombinant adeno-associated virus comprising an AAV serotype capsid protein or a gene encoding human apolipoprotein E (apoE) or apoA.
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apolipoprotein E; apoE; apolipoprotein A; apoA; atheroscleros
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OVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRP 598
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                                                      IWAKIPHTDGHFHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
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                                                                                                          VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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RESULT 10
ADZ27074
rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; bacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; antipsoriatic; vasotropic; gastrointestinal-gen.;
                                                                           antiarthritic; neuroprotective; antiinflammatory;
antipsoriatic; vasotropic; gastrointestinal-gen.;
virucide; antibacterial; cytostatic; antiulcer; de
                                            Adeno-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
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                IWAKI PHTDGHFHPS PLMGGFGLKNPPPPQILI KNTPVPANPPAEFSATKFAS FITQYSTG
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IWAKI PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
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                              New adeno-associated virus (AAV) clade comprising at least three members, useful for preventing and/or treating arthritis, multipl sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bac
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KW ather
                                                                                                                            AAB59847 standard;
                                                AAV6 capsid protein
                                                                            28-MAR-2001
 gene therapy; AAV viral vector; cystic fibrosis; osclerosis; sickle cell anaemia; thalassaemia; clotting disorder; diabetes; capsid protein VP1.
                                                                          (first
                                                                                                                             protein;
                                                    VΡ1
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QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL

736

clotting disorder;

AIDS;

SEQ

ij

NO 158;

569pp;

English

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Query Match
Best Local Simi
Matches 594;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adeno-associated virus serotype 6 and viral vector derived from it gene therapy of cystic fibrosis, cancer, acquired immunodeficiency syndrome, sickle cell anemia, thalassemia and diabetes.
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                                                                                                                                                                            NSNFTWTGASKYNLNGRESI INPGTAMASHKDDEDKFFPMSGVMI FGKESAGASNTALDN
                                                                                                                                                                                                                                     LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
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IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
                                                                VMITDEEEIKATNPVATERFGTVAVNLQSSSTDPATGDVHVMGALPGMVWQDRDVYLQGP
                                                                                            VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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Pred. No. 8.3e
3; Mismatches
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TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAA

Query Match Best Local S Matches 594

al Similarity 594; Conser

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Score 3229; DB 7; Pred. No. 8.3e-252; 3; Mismatches 2;

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                                                    The invention relates to a novel method for detecting adeno-associated CC virus (AAV) sequences in a sample, which comprises subjecting a sample CC containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cyrostatic, antirheumatic, antiarthritic, neuroprotective, antignoriatic, antirhyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other autoimmune diseases (like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune trhyroiditis, scleroderma or Crohn's disease. This sequence represents an C AAV related protein sequence of the invention.
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17-DEC-2001;
01-MAY-2002;
05-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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2001US-0341117P.
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                                                                             19-JUN-2003; : 30-APR-2004; : 03-JUN-2004;
                                                                                                                                                                                                                                                     immunosuppressive; gene therapy; immunogenicity; virus inactivation; hemophilia; Pepck deficiency; galactosemia; phenylketonuria; Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia; atherosclerosis; thrombosis; embolism; Parkinson's disease; congestive heart failure; cancer; inflammation; immune disorder;
                                                                                                                                                                                                                 Adeno-associated
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                             Arbetman AE,
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New mutated adeno-associated virus (AAV) capsid protein that when present in an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding wild-type virion, useful for treating e.g.

SEQ ID NO 19; 136pp; English

delivering a recombinant AAV virion to a cell or tissue of a vertebrate subject. The recombinant AAV virion is useful for delivering a heterologous nucleic acid molecule to a cell or tissue of a vertebrate subject. Where the protein encoded by the heterologous nucleic acid molecule is expressed at a level that provides a therapeutic effect, where the recombinant AAV virion may comprise a non-primate, mammalian where the protein that when present in an AAV virion imparts decreased immunoreactivity to the virion as compared to immunoreactivity of primate AAV-2, and the heterologous nucleic acid molecule, where the heterologous immunoreactivity to the virion as compared to the corresponding wild-type virion. Also described are: a polynucleotide encoding the mutated protein above; a recombinant AAV virion comprising the mutated protein above; and Nyan syndrome, Zellweger syndrome, ischemic diseases, atherosclerosis, thrombosis, embolisms, Parkinson's disease, congestive heart failure, cancer, inflammatory and immune disorders, muscular dystrophies, and diabetes. This is the amino acid sequence of adeno-associated virus 6 nucleic acid molecule encodes a therapeutic protein and is operably linked to control elements capable of directing the in vivo transcription and translation of the protein. The protein or the recombinant AAV virion is useful for treating or preventing a wide variety of disorders such as hemophilia, glycogen storage deficiency type 1A, Pepck deficiency, galactosemia, phenylketonuria, Crigler-Najjar disease, Gout and Lesch-Nyan syndrome, Zellweger syndrome, ischemic diseases, atherosclerosis, protein that when present invention protein describes a amino acid sequence of adeno-associated virus 6 VP1. in an AAV virion mutated adeno-associated sociated virus (AAV) imparts decreased capsid

Sequence

Query Match Best Local Matches 59	/ Match 99.3%; Score 3229; DB 9; Length 736; Local Similarity 99.2%; Pred. No. 8.3e-252; 1es 594; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAA 60	
מם	138 TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAA 197	
Qy	61 VGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLY 120	
Дb	198 VGPTTWASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLY 257	
Qy	121 KQISSASTGASNDNHYFGYSTFWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLF 180	
DЬ	SPRDWQRLINNNWGFRPKR	
Qy	181 NIQVKEVTTNDGVTTTANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG 240	
Db	318 NIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG 377	
Qy	241 YLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNP 300	
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Qy	301 LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN 360	
Db	438 LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN 497	
Qy	361 NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDN 420	
Db	498 NSNFTWTGASKYNLNGRESIINPGTAMASHKDDKDKFFPMSGVMIFGKESAGASNTALDN 557	
Qγ	421 VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGF 480	
Дb	558 WITDEEEKATNPVATERFGTVAVNLQSSSTDPATGDVHVMGALPGMVWQDRDVYLQGP 617	
γQ	481 IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG 540	

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Db 618 IWAKIPHTDGHFHPSPLWGGFGLKHPPPQILIKNTPVPANPPABFSATKFASFITQYSTG 677 Qy 541 QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 599 Db 678 QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736 Search completed: November 23, 2005, 17:35:12

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Post-processing: Minimum Match 0%
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C;Species: adeno-associated virus type 2
C;Species: adeno-associated virus type 2
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul
C;Accession: A03698
R;Srivastava, A.; Lusby, E.W.; Berns, K.I.
J. Virol. 45, 555-564, 1983
A;Title: Nucleotide sequence and organization of the adeno-associated A;Reference number: A03694; MUID:83164299; PMID:6300419
A;Accession: A03698
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A;Molecule type: DNA
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A;Residues: 1-504 <SRI>
A;Residues: 1-504 <SRI>
A;Cross references: UNIPROT: P03135; UNIPARC: UPI0000127C8E; EMBL: J01901; NID: g209616;
C;Superfamily: adeno-associated virus coat protein
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                                                       EEEIGTTNFVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYLQGFIWAKI
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Database

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09-Jul-2004

virus 2 genome

M.; Stout, E.R.; Bates, R.C.

of bovine

parvovirus

Length 673; Indels 144;

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EMBL: M14363;

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A;Gene: VP1
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A; Accession: $52210
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R;Zadori, Z.; Erdei, J.; Nagy, J.; Kisari, submitted to the EMBL Data Library, Septem
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A; Residues: 1-732 <ZAD>
                                                        밁
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;Species: muscovy duck parvovirus
;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keywords: coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: parvovirus coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                       E--SAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALKFKIFNVQVKEVTTQDQTKTIANNLTSTIQIFTDNEHQLFYVLGSATEGTMPPFPSDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRPVEQSPQEPDSSSGIGK-TGQQPAKKRLNFGQTGDSESVPDPQPLG---
                                                                                                                                 NQKWNSYITQYSTGQCTVEMVWELRKENSKRWNPEIQFTSNFGNRTSTMFAPNETGGYVE
                                                                                                                                                     ATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTE
                                                                                                                                                                                                                                   GMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFS
                                                                                                                                                                                                                                                                                    DPYRSGSTLAGISDIMVTDEQEIAPTNGVGWRPYGLTVTNEQNTTTAPTNAELEVLGALP
                                                                                                                                                                                                                                                                                                                                                                                                    RVSKTK--TDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGK 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YALPOYGYCTMHTNOSGARFNDRSAFYCLEYFPSOMLRTGNNFEFSFEFEEVPFHSMFAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNNHMYQAITSGTNPDSN-TQYAGYSTPWGYFDFNRFHCHFSPRDWQRLINNHWGIRPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEPVNTAPAKKSS----GKLTDHDPIVKKPKLSE----ENSPSPSNSGGEASAAATEGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTG
                                                          DRLIGTRYLTQNL
                                                                                            PRPIGTRYLTRPL 599
                                                                                                                                                                                                           GMVMQNRDIYLQGPIWAKIPKTDGKPHPSPNLGGFGLHNPPPQVFIKNTPVPADPPLEYV
                                                                                                                                                                                                                                                                                                                                                                RVRAYSGGTDNYANWSIWSKGNKVFLKDREYLLQPGPVATTHTEDQASSVPAQNIIGIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                         SQDLDRLMNPLLDQYLWNFSEV-NGGRNAQ-----FKKAVKGAFGAMGRNWLPGPKLLDQ
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                                                            732
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Pred. No. 1.6e-108;
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N;Contains: coat protein VP2
C;Species: bovine parvovirus
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_chang
C;Accession: A26104
R;Chen, K.C.; Shull, B.C.; Moses, E.A.; Lederman, M.; Stout, E
J. Virol. 60, 1085-1097, 1986
A;Title: Complete nucleotide sequence and genome organization
A;Seference number: A26104; MUID:87061184; PMID:3783814
A;Accession: A26104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-673 <CHS>
A;Cross-references: UNIPROT:P07297; UNIPARC:UPI0000127D77;
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
C;Keywords: coat protein VP2 #status predicted <VP2>
coat protein VP1 - parvovirus B19 (stra C;Species: parvovirus B19 (stra A;Note: host Homo sapiens (man) C;Date: 28-Dec-1987 #sequence_revision
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Best Local Sim
Matches 160;
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Local Similarity 25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEP--PATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYNLQIKQIMTDGAMGTVYNNDLTAGMHIFCDGDHRYPYVQHPWDDQCMPELPNSIWELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGPRPKRLNFK 178
                                                                                                                                                       EIEWELQKENSKRWNPEVQYTSNYAKSANVD-FTVDNNGLY
                                                                                                                                                                                                                                                                                                        -----AARHTFTREARTKLITGSNGADGDYKEWWMLPNQMWDSAPISRYNPIWVKVP
                                                                                                                                                                                                                                                                                                                                                                                  NGAD----VSGVRAVRVGYSTDPIYGGQQPESDLLRLRYSASAAEGQQNPILEN-----
                                                                                                                                                                                                                                                                                                                                                                                                                       DDEDKFFPMSGVM------IFGKE------SAGASNTALDNVMITDE
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                                                                                                                                                                                                                                                                  HTDGHFHPSPLMGGFGLKNPPPQILIK--NTPVPANPPAEFSATKFASFITQYSTGQVSV 544
                                                                                                                                                                                                                                                                                                                                               EEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYAHSQSLDRLMNPLIDQYLYYLNRTQN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 556; DB 1;
Pred. No. 3.4e-30;
                                                            (strain
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     28-Dec-1987
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-GIARGTHNATLQTQSAGALVTMVT

426 462

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564

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OSGSAONKDLLFSRGSP-----

329

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424 331 373

#text_change 09-Jul-2004

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A;Cross-references: UNIPROT:P07299; UNIPARC:UPI0000127D7C; C;Superfamily: parvovirus coat protein C;Keywords: coat protein
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R;Shade, R.O.; Blundell, M.C.; Cotmore,
J. Virol. 58, 921-936, 1986
                                                  coat protein VP1 - porcine parvovirus
N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Sate: 30-Sep-1991 #sequence_ revision 30-Sep-1991 #text_change 09
C;Accession: B33302
C;Accession: Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A;Title: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971
A;Accession: B33302
A;Molecule type: DNA
A;Residues: 1-723 - RNN
A;Residues: 1-724 - RNN
A;Residues: 1-725 - RN
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Best Local S
Matches 148
Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSAHQGCLPPFPADVFMIPQYGYLTLNN-GSQAVG-----RSSFYCLEYFPSQMLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRLINNNWGFRPKRLNFKLFNIQVKEVT--TNDGVTTIANNLTSTVQVFSDSEYQLPYVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FPNKGTQQYTDQIE-RPLMVGSVWNRRALHYESQLWSKIPNLDDSFKTQFAALG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASHKDDEDKFFPMSGVMIFGKESAGASNTALDNV-----MITDEEEIKATNPVATERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTASMSYKFPPVPPENLEGCSQHFYEMYNPL---YGSRLGVPDTLGGDPKFRSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -THEDHAI OPONEMPGPLVNSVSTKEGDSSNTGAGKALTGLSTGTSONTRISLRPGPVSO
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                                  UNIPROT: P18546;
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                                  UNIPARC: UPI0000174964;
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No. 6.2e-26;
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                                  EMBL: D00623
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A;Introns: 10/1
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;145-723/Product: coat protein VP2 #s
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Best Local Similarity
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                                                                 DDFNADSPOOPRIITYSNFWWKGTLTFTAKMRSSNMWNPIOOHTT--
                                                                                                                                                                                                                                                                                                                                                                         QNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTYNNHLYKQI-----SSASTGAS-NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINN
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                               GLYTEPRPIG
                                                                                                                                      LTALINITAPVFPNGQIWDKELDTDLKPRLH---VTAPFVCKNNPPGQLFVKIAP---
                                                                                                                                                                                                                                                                                                                                           NTRKGYHOTINNSYTEAT ---- AIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                              SQMLRTGNNF-TFSYTFEEVPFHSSYAHSQSLDR-----LMNPLI--DQYLYYLNRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCLPPFPADVFMI PQYGYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTEINLVSFEQAIFNVVLKTITESATSPPTKIYNNDLTASLMVALDTNNTLPYTPAAPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWGFRPKRLNFKLENIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMPEHETYKRIHVLNSESGSAGQMVQDDAHTQMVTPWSLIDANAWGVWFNPADWQLISNN
GKYI-PTNIG
                                                                                                  AEFSA-TKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNN
                                                                                                                                                                                                       ELERYTFNPQSKCGRAPKQQFNQQAPLNLENTNNGTLLPSDPIGGKSNMHFMNTLNTYGP
                                                                                                                                                                                                                                        EIK--ATNP-----VATERFGTVA-VNFQSSS-----TDPATG--DVHAMGALP----
                                                                                                                                                                                                                                                                            ------GAIRFTMDYQHGHLTTSSQ
                                                                                                                                                                                                                                                                                                          NLNGRESIINP--GTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD---NVMITDEE
                                                                                                                                                                                                                                                                                                                                                                                                             IHLLRTGDEFSTGIYHFDTKPL--KLTHSWQTNRSLGLPPKLLTEPTTEGDQHPGTLPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETLGFYPWLPTKPTQYRYYLSCIRNLNPPTYTGQSQPNNRLNTNRLHSDIMFYTIENAVP
                                                                                                                                                                     -GMVWQDRDVYLQGPIWAKIPHTD--GHFHPSPLMGGFGLK-NPPPQILIKNTPVPANPP
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Pred. No. 8.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TLNNGSOAVGRSS-----FYCLE-YFP
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C;Species: porcine parvovirus
C;Date: 30-Sep-1993 #text_change 09-Jul-2004
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A60006
R;Sakurai, M.; Nishimori, T.; Ushimi, C.; Nakajima, H.
Virus Res. 13, 79-86, 1989
Virus Res. 13, 79-86, 1989
A;Title: Nucleotide sequence of capsid protein gene of porcine parvovirus.
A;Reference number: A60006; MUID:89319168; PMID:2750278

A; Molecule type: I A; Residues: 1-729

DNA

<SAK

A; Accession: A60006

A;Cross-references: UNIPROT:P33484; UNIPARC:UPI0000127C6E

RESULT 6 A60006

coat protein VP1 - porcine parvovirus
N;Contains: coat protein VP2

(strain 90HS

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coat protein VP1 - porcine parvovirus (strain NADL-2)
N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
C;Accession: B33743; D48472
C;Accession: B33743; D48472
R;Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 173, 368-377, 1989
A;Title: Nucleotide sequence analysis of the capsid genes and th
A;Reference number: A33743; MUID:90085785; PMID:2596019
A;Accession: B33743
                                                                                                                                                                                                                                 RESULT
VCPVNA
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A; Molecule type: DNA
A; Residues: 1-729 < VAS>
A; Cross-references: UNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QMLRTGNNF-TFSYTFEEVPFHSSYAHSQSLDR-----LMNPLI--DQYLYYLNRTQ
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   UNIPROT: P18546; UNIPARC: UPI0000127C70; GB: M32787; NID: g332983;
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22.7%; Pred. No. 1.6
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R;Bergeron, J.; Menezes, J.; Tijssen, P.

Virology 197, 86-98, 1993
A;Title: Genomic organization and mapping of transcription and translati
A;Reference number: A48472; MUID:94025614; PMID:8212598
A;Reference number: A48472; MUID:94025614; PMID:8212598
A;Rocession: D48472
A;Molecule type: DNA
A;References: UNIPARC:UPI0000174965
A;Cross-references: UNIPARC:UPI0000174965
A;Experimental source: NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:13879
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:13879
C;Genetics:
A;Introns: 10/1
C;Superfamily: parvovirus coat protein
C;Reywords: coat protein; glycoprotein
C;Reywords: coat protein; glycoprotein
C;Reywords: coat protein; glycoprotein
F;151-729/Product: coat protein VP2 #status predicted <VP2>
F;32,172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asm
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                                      LYTEPRPIG
                                                            DENADSPOOPRIITYSNEWWKGTLTETAKMRSSNMWNPIQOHTT-
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                                                                                                               EFSA-TKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNG
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  NYI-PTNIG
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22.7%;
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Pred. No. 1.6e-09;
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C;Species: parvovirus H1
A;Note: host Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change (C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change (C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text_change (C;Date: 14-Nov-1983 #sequence (T;Date: 14-Nov-1983)
R;Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nucleotide sequence of H-1 and mappin A;Reference number: A03695; MUID:83112183; PMID:6823009
A;Accession: A03699
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A;Residues: 1-722 <RHO>
A;Cross-references: UNIPROT:P03136; UNIPARC:UPI0000127D7D;
C;Superfamily: parvovirus coat protein
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RESULT 9
844276
coat protein VP1 - parvovirus LuIII
C;Species: parvovirus LuIII
C;Date: 17-Feb-1994 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                         KDDEDKFFPMSGVMIFGKESAGASNTALDNVMITDEEEIKA-TNPVATERFGTVAVNFQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 244; DB 1;
Pred. No. 8.4e-09;
   17-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                   IYPNGQIWDKELDLEHKPRLHVTAPFV---CKNNP
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A;Reference number: A44276; MUID:93297126; PMID:8517025 A;Accession: B44276
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R;Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, Virology 192, 339-345, 1993
A;Title: The complete nucleotide sequence of par
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A; Residues: 1-587 < DIF>
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APNLTDQYDPNSSNLSRIVTYGTFFWKGKLTLKAK---MRPNA-TWNPVFQISA
                                                                                                                                                                                                                                                                               SGLTQIQGRNDVTEATRVRPAQVGFCQPHDNFETSRAGPFKVPVVPADITQGLDHDANGS
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                                TP--VPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTS
                                                                                                                                                                       VMIFGKESAGASNTALDNVMITDEEEIKATNPVATER---FGTVAVNFQS--SSTDPATG
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                                                                                                                                      -WTNNCFIQSVPFTSEPN---ANQILTNRDNLAGKTDIHFTNAFNSYGPLTA
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Pred. No. 3e-01
74; Mismatches
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R;Astell, C.R.; Thomson, M.; Merchlinsky, M.; Ward, D.C. Nucleic Acids Res. 11, 999-1018, 1983
A;Title: The complete DNA sequence of minute virus of mice, A;Reference number: A03696; MUID:83143341; PMID:6298737
A;Accession: A03700

an

autonomous

parvovirus

A; Molecule type: DNA A; Residues: 1-716 < AST>

A;Cross-references: UNIPROT: P03137; UNIPARC: UPI0000127D6D;

EMBL: V01115

coat protein VP1 - minute virus of mice
C;Species: minute virus of mice, murine parvovirus
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983

#text_change 09-Jul-2004

Accession: A03700

VCPV2M

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J. Virol. 55, 574-587, 1985
A;Title: Cloning and sequence of DNA encoding structural proteins of the autonomous p A;Reference number: A03697; MUID:85265017; PMID:2991581
A;Accession: A03701
A;Molecule type: DNA
A;Residues: 1-727 <CAR>
A;Cross-references: UNIPROT:P04864; UNIPARC:UPI0000127D55; EMBL:M10824; NID:g333474; A;Introns: 11/1
                                                                                                                 coat protein VP1 - feline panleukopenia virus R;Contains: coat protein VP2 C;Species: feline panleukopenia virus, FPLV C;Date: 30-Jun-1987 #sequence_revision 30-Jun C;Accession: A03701 R;Carlson, J.; Rushlow, K.; Maxwell, I.; Maxw J. Virol. 55, 574-587, 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QPLGEPPA--TPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDS--TWLGD---R
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                                                                                                                                                                                                                                                                                                    NPEVQYTSNYAKSANVDFTVDNNGLY---TEPRPIGT-----RYLTRPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSSFYCLEYFPS-QMLRTGNNF-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYY
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                                                                                                                                                                                                                                                                                                                                                             FGLKNPPPQILIKNTP--VPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRW
                                                                                                                                                                                                                                                                                                                                                                                           HFSNVFNSYGPLTAFSH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPG-------
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                                                                                                                                                                                                                                                                                                                                 -CKNNAPGQMLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - PEADTDAGT-----LTAQGSRHGTTQMGVNWVSEAIRTRPAQVGFCQPHNDFEASRAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMSGVMIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 216; DB 1;
Pred. No. 6.9e-07;
                                                                                                                                                                                                                                                                           -DNGNSYMSVTKWLPTATGNMQSVPLITRPV
                                                                                                                                                                                                                                                                                                                                                                                           ----PSPVYPQGQIWDKELDLEHKPRLHITAPFV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 271; Indels
                                                                                                                                I.; Maxwell, F.; Winston,
                                                                                                                                                        FPLV
30-Jun-1987 #text_change
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                                                                                                                                S.; Hahn,
                                                                                                                                                            09-Jul-2004
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R;Sahli, R.; McMaster, G.K.; Hirt, B.

Nucleic Acids Res. 13, 3617-3633, 1985

A;Title: DNA sequence comparison between two tissue-specific variants of the autonom A;Title: DNA sequence comparison between two tissue-specific variants of the autonom A;Reference number: A23008; MUID:85242059; PMID:3855242

A;Accession: B23008

A;Accession: B23008

A;Molecule type: DNA

A;Residues: 1-718 <SAH>
A;Residues: 1-718 <SAH>
A;Residues: UNIPROT:P07302; UNIPARC:UPI0000174963; EMBL:X02481; NID:g60918; R;Astell, C.R.; Gardiner, E.M.; Tattersall, P.

J. Virol. 57, 656-669, 1986
                                                                                                                                                                                                                                                                    coat protein VP1 - minute virus of mice (strain MVMi)
C;Species: minute virus of mice, murine parvovirus
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: B23008; B29510
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C;Keywords: coat protein
F;144-727/Product: coat protein VP2 #status predicted <VP2>
                                                                                                                                                                                                                                                                                                                                                                                  VCPVIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPESENYKRVVVNNMDKTAVKGNMALDDTHVQIVTPWSLVDANAWGVWPNPGDWQLIVNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVMIFGKESAGASNTALD-NVMITDEBBIKATNPVATERFGTVAVNFQSSSTDPATGDVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGSAQNKDLLFSRGSPAGMS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GRYPAGDWIQNINFNLPVTNDNVLLPTDPIG----GKTGINY--TNIFNTYGPLT
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Pred. No. 7e-07;
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coat protein VP1 - mink enteritis virus (strain )
NyContains: coat protein VP2
C;Species: mink enteritis virus, MEV
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-199
C;Accession: B38350
R;Kariatsumari, T; Horiuchi, M.; Hama, E.; Yagua
J. Gen. Virol. 72, 867-875, 1991
A;Title: Construction and nucleotide sequence and A;Reference number: A38350; MUID:91202123; PMID:
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A;Reference number: A29
A;Reference number: A29
A;Accession: B29510
A;Molecule type: DNA
A;Residues: 1-143,'A', I
A;Residues: 1-143,'A', I
A;Cross-references: UNI
C;Superfamily: parvovir
C;Keywords: coat protei
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Best Local S
Matches 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keywords: coat protein
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                                                                                                                                                                                                                                                                                                                                                                                                           GPLTAFSH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRSSFYCLEYFPS-QMLRTGNNF-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYQLPYVLGSAHQGCLPPFPADVFMIPQYGY-----LTLNN------GSQAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITALATRL VHLNMPKSENYCR I RVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAWGVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VITTSTRTWALPTYNNHLYKOI------SSASTGASNDNHYFGYSTPWGYFDFNRFHCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----EPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDS--TWLGD---R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKLATDSEP-GTSGVSRAGKRTRPPAYIFINQARAKKKLTSSAAQQSSQTMSDGTSQPDG
                                                                                                                                                                                                                                                                                                                                MLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRA----NTTWNPVYQ----
                                                                                                                                                                                                                                                                                                                                                                   ILIKNTP---VPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                               DPATGDVHAMGALPGMVWQDRDVYLQGPIWAK---IPHTDGHFHPSPLMGGFGLKNPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- FPMSGVMIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GP-FAAPKVPADVTQGVDREANGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --PEADTDAGT----LTAQGSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRA
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                                                                                                                                                                                                                                                                                            YAKSANVDFTVDNNG
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Pred. No. 8.7e
89; Mismatches
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1. No. 8.7e-07;
1. no. 8.7e-273;
                                                                                                 30-Jun-1992 #text_change 09-Jul-2004
                                                                                                                                                         (strain
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pMID:3502703
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     nce analysis of PMID:2016597
                                                           Yaguchi, K.; Ishigurio, N.;
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                             of the
                                                                 Shinag
                                                                                                   coat protein VP1 - feline panleukopenia virus NyContains: coat protein VP2 C;Species: feline panleukopenia virus, FPLV C;Date: 31-Dec-1991 #sequence_revision 31-Dec-C;Accession: B36608
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C;Keywords: coat protein
F;139-722/Product: coat protein VP2 #s
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A;Molecule type: DNA
A;Residues: 1-722 <KAR>
A;Cross-references: UNIPROT:P27437; UNIPARC:UPI0000174967; GB:D00765
       R;Martyn, J.C.; Davidson, B.E.;
J. Gen. Virol. 71, 2747-2753, 19
A;Title: Nucleotide sequence of
A;Reference number: A36608; MUID
A;Accession: B36608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPESENYKRVVVNNMDKTAVKGNMALDDTHVQIVTPWSLVDANAWGVWFNPGDWQLIVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPTKRSKPPPHIFINLAK-----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSELHLVSFEQEIFNVVLKTVSESATQPPTKVYNNDLTASLMVALDSNNTMPFTPAAMRS
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                                                                                                                                                                                                                                                                                SIN----
                                                                                                                                                                                                                                                                                                                                                                                         POILIKNTPVPAN---PPAEFSATKFASFITOYSTGOVSVEIEWELQKENSKRWNPEVOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVMIFGKESAGASNTALD-NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGRGGAQTDENQAA----DGDPRYAFGRQHGQKTTTTGETPERFTYIAHQDT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWGFRPKRLNFKLENIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
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                                                                                                                                                                                                                                                                                                                  TSNYAKSANVDFTVDNNGLYTEPRPIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ALNNVP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TKTDNNNSNFTWTGASKY---NLNGRESIINPGT----AMASHKDDEDKFFPMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 101;
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                                                                                                                                                                                                                                                                                ----VDNQFNYL-PNNIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     --- PVY PNGQI WDKE FDTD
                                 e of feline panleukopenia virus:
MUID:91073139; PMID:2174965
                                                                       1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GGGSGGVGISTGTFNNQTEFKFLENGWV--EITANSSRLVHLN
                                                                                 Studdert, M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 214; DB 1;
Pred. No. 9.5e-07
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                                                                                                                           FPLV
31-Dec-1991
                                                                                                                                                                                                                                                                                705
                                                                                                                                                                                                                                                                                                                      591
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                                                                                                                               09-Jul-2004
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canine

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A;Molecule type: DNA
A;Residues: 1-727 <max>
A;Residues: 1-727 <max>
A;Cross-references: UNIPROT:P24840; UNIPARC:UPI0000127D56; GB:X55115
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;144-727/Product: coat protein VP2 #status predicted <VP2>
                                                                                              coat protein VP1 - canine parvovirus (strain CPV-d)
%;Contains: coat protein VP2
C;Species: canine parvovirus, CPV
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990
C;Accession: A31163
                                                                                                                                                                                RESULT
VCPVCD
                 A; Title: Canine host range and a specific epitope map along A; Reference number: A31163; MUID:89020796; PMID:3176341 A; Accession: A31163
                                                             R;Parrish, C.R.; Aquadro, C.F.;
Virology 166, 293-307, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCL-----PPFPA-----SFYCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSELHLVSFEQEIFNVVLKTVSESATQPPTKVYNNDLTASLMVALDSNNTMPFTPAAMRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPESENYKRVVVNNMDKTAVKGNMALDDIHVQIVTPWSLVDANAWGVWFNPGDWQLIVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYNNHLYKQI-----SSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGSGNGSGGGG------GGGSGGVGISTGTFNNQTEFKFLENGWV--EITANSSRLVHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGPTTMASGGGAPMADNNEGADGVGNASGNWH-----CDSTWLGDRVITTSTRTWALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPTKRSKPPPHIFINLAK-----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVP----DPQPLGEPPA--TPAA
                                                                                                                                                                                                                                                  SIN----
                                                                                                                                                                                                                                                                               TSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                                                                                                                                                                                                                GQLFVKVAPNLTNEYDPDASANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQM
                                                                                                                                                                                                                                                                                                                                                POILIKNTPVPAN---PPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQY
                                                                                                                                                                                                                                                                                                                                                                                 ALNNVP-----PVYPNGQIWDKEFDTD
                                                                                                                                                                                                                                                                                                                                                                                                               AMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVM1FGKESAGASNTALD-NVM1TDEBE1KATNPVATERFGTVAVNFQSSSTDPATGDVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E-YFPSQMLRTGNNF-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETLGEYPWKPTIPTPWRYYFQWDRTLIPSH-----TGTSGTPTNVYHGTDPDDVQFYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NWGFRPKRLNFKLFNIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGRGGAQTDENQAA----DGDPRYAFGRQHGQKTTTTGETPERFTYIAHQDT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TKTDNNNSNFTWTGASKY---NLNGRESIINPGT----AMASHKDDEDKFFPMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGATNFGDIGVQQDKRRGVTQMGNTDYITEATIMRPAEVGYSAPYYSFEASTQGPFKTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENSVPVHLLRTGDEFATGTFFFDCKP--CRLTHTWQTNRALGLPP----FINSLPQS
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                                                                                                                                                                                                                                                  ----VDNQFNYV-PNNIG
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                                                                                Carmichael,
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Pred. No. 2.1e-06;
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A;Residues: 1-737 <PAR>
A;Cross-references: UNIPROT:P17455; UNIPARC:UPI0000127D7A; EMBL:M23255; NID:g333467; PID
C;Genetics:
A;Introns: 26/3
A;Introns: 26/3
C;Superfamily: parvovirus coat protein
C;Superfamily: parvotein
C;Keywords: coat protein
C;Keywords: coat protein
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les 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPTKRSKPPPHIFINLAK-----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCL-----PPFPA------DVFMIPQYGYLTLNNGSQAVGRS-----SFYCL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPESENYRRVVVNNMDKTAVNGNMALDDIHAQIVTPWSLVDANAWGVWFNPGDWQLIVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVP----DPQPLGEPPA--TPAA
                                                                  CONNCPGOLFVKVAPNLTNEYDPDASANMSR----IVTYSDFWWKGKLVFKAKLRASHTW
                                                                                                                                                                                                                                                                                                                                                                                                          ENSVPVHLLRIGDEFATGTFFFDCKP--CRLTHTWQTNRALGLPP-----FLNSLPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSELHLVSFEQEI FNVVLKTVSESATQPPTKVYNNDLTASLMVALDSNNTMPFTPAAMRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWGFRPKRLNFKLFNIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGPTTMASGGGAPMADNNEGADGVGNASGNWH-----CDSTWLGDRVITTSTRTWALP
                                 NPEVOYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                   ---NPPPQILIKNTPVPAN---PPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRW
                                                                                                                                   TYGPLTALNIVP-----PVYPNGQIWDKEFDTD---
                                                                                                                                                                    ATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK------
                                                                                                                                                                                                    ERFTYIAHQDTGRYPEGDWIQNINFNLPVTNDNVLLPTDPIG----GKTGINY--TNIFN
                                                                                                                                                                                                                                                                                                                                         EGATNFGDI ------GV--
                                                                                                                                                                                                                                                                                                                                                                       SGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNF-----TW
                                                                                                                                                                                                                                                                                                                                                                                                                                        E-YFPSQMLRTGNNF-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQ 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETLGFYPWKPTIPTPWRYYFQWDRTLIPSH-----TGTSGTPTNIYHGTDPDDVQFYTI
NPIQQMSIN-
                                                                                                                                                                                                                                                                     VGYSAPYYSFEASTOGPFKTPIAAGRGGAQTDENQAADGNPRYAFGRQHGQKTTTTGETP
                                                                                                                                                                                                                                                                                                        TGASKYNLNGRESIINP----GTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 208; DB 1; I; pred. No. 2.5e-06; 96; Mismatches 260;
   VDNQFNYV-PSNIG
                                                                                                                                                                                                                                     ----NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDP
                                                                                                                                                                                                                                                                                                                                         QQDKRRGVTQMGNTNYITEATIMRPAE
                                    591
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Search completed: November 23, 2005, 17:44:02 Job time: 23.1525 secs

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Run š

protein

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protein search, using

88

model

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

November 23,

Sequence: Title: Perfect score:

US-10-696-282-15 3251

1 TAPGKKRPVEQSPQEPDSSS.....

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

2166443 seqs,

705528306 residues

chosen parameters:

2166443

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3662.868 Million cell updates/sec
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Q$MBPB $VIRU

Q$MBPB;

AC Q$MBPB;

DT 01-NOV-1999 (TrEMBLrel. 12, Li
DT 01-NOV-1999 (TrEMBLrel. 26, Li
DT 01-MAR-2004 (TrEMBLrel. 26, Li
DT 01-MAR-2004 (TrEMBLrel. 26, Li
DT 01-MAR-2004 (TrEMBLrel. 26, Li
DE Capsid protein.

OS Adeno-associated virus 1.

OC Viruses; ssDNA viruses; Parvov

OX NCBL_TaxID=85106;

RN NUCLEOTIDE SEQUENCE.

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MEDLINE-99214338; PubMed=10196295;
MEDLINE-99214338; PubMed=10196295;
MEDLINE-99214338; PubMed=10196295; McCullough B., Ga''''

"Gene therapy vectors based on adeno-associated vir''
J. Virol. 73:3994-4003(1999).

EMBL; AF063497; AAD27757.1; -; Genomic_DNA.

EMBL; AF063497; AAD27757.1; -; Genomic_DNA.

SMR; Q9WBPB; 217-736.

RGO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; F:structural molecule activity; IEA

RGO; GO:0005198; F:structural molecule activity; IEA

RGO; GO:00190283; C:viral capsid; IEA.

RGO; GO:00190284; C:viral capsid; IEA.

RGO; GO:00190285; C:viral capsid; IEA.

RGO; GO:00190286; C:vira
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Best Local Similarity
Matches 599; Conserv
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NCE 736 AA; 81375 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLY
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                                                          LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
                                                                                     LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
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Pred. No. 5.1e-216;
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virus type 1.";
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UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Result No.

Score

Match Query

Length

BB

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SUMMARIES

Q6JC10_9VIRU Q6JC13_9VIRU O56139_9VIRU

Q9WBP8_9VIRU Q6JC08_9VIRU Q6JC12_9VIRU O56137_9VIRU

Q6jc08 Q6jc12 O56137

Q67008 9VIRU
Q64024 9VIRU
Q64027 9VIRU
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Wilson J.
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SMR; GG1C08; 217-736.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 736 AA; 81317 MW; 373C7C40975CD9BD
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05-JUL-2004 (TrEMBLrel.
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PubMed=15.63731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=272636;
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NSNFTWTGASKYNLNGRESI I NPGTAMASHKDDEDKFFPMSGVMI FGKESAGASNTALDN
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                                             LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
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J. Virol.
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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EMBL; AY530607; AAS99292.1; -;
SMR; Q6JC12; 217-736.
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Viruses; ssDNA viruses;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; GO; GO:00740; Parvo_coat.
Pfam; PF00740; Parvo coat; 1.
SEQUENCE 736 AA; 81411 MW; 311217A089C565F5
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MEDLINE=98080418; PubMed=9420229;

Rutledge E.A., Halbert C.L., Russell D.W.;

"Infectious clones and vectors derived from

(AAV) serotypes other than AAV type 2.";

J. Virol. 72:309-319(1998).
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                                                                        NIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG
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                       NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDN
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J. Virol. 78:6381-6388(2004).
EMBL; AY530609; AAS99294.1; -; Genomic_I SMR; Q6JC10; 217-736.
GO; G0:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule ad InterPro. IPRO01403; Parvo Coat.
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QGJC10;
05-JUL-2004 (TrEMBLrel. 27,
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05-JUL-2004 (TrEMBLrel. 27,
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Wilson J.
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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                                                                                  LIDQYLYYLNRTQNQSGSAQNRDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
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"Clades of Adeno-associated viruses are tissues.";
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78:6381-6388(2004).
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 737 AA; 81332 MW; 94CED0F3AFD6E492
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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EMBL; AY53606; AAS99291.1; -; Genomic_DNA
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                   NNSNFTWTGASKYNLNGRES I INPGTAMASHKDDEDKFFPMSGVMI FGKESAGASNTALD
                                                                                       PLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDN
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   NNSNFTWTGASKYNLNGRESI I NPGTAMASHKDDEDKFFPMSGVMI FGKESAGASNTALD
                                                                  PLIVQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDN
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Pred. No. 5.7e-210;
6; Mismatches 9;
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Matches 514
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01-JUN-1998 (TREMBL
01-MAR-2004 (TREMBL
Capsid protein VP1.
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Viruses; ssDNA viruses;
VCBI_TaxID=68742;
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9VIRU
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Local Similarity 85.7%;
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NUCLEOTIDE SEQUENCE.
MEDINE=98080418; PubMed=9420229;
MEDINE=98080418; PubMed=9420229;
Rutledge E.A., Halbert C.L., Russell D.W.;
"Infectious clones and vectors derived from
"Infectious clones and vectors derived from
(AAV) serotypes other than AAV type 2.";
J. Virol. 72:309-319(1998).
EMBL; AF028705; AAB95452:1; -; Genomic_DNA.
SMR; 056139; 217-736.
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SEQUENCE 736 AA; 81906 MW; DD52331AD5F0D70F CRC64;
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                                                                                                               LIDQYLYYLNRTQ-NQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDN
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                  NNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD
                                                                                                                                                                                                     YLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNP
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                                                                                     LIDQYLYYLNRTQGTTSGTTNQSRLLFSQAGPQSMSLQARNWLPGPCYRQQRLSKTANDN
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NNSNFPWTAASKYHLNGRDSLVNPGPAMASHKDDEEKFFPMHGNLIFGKEGTTASNAELD
                                                                                                                                                                              YLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYTFEDVPFHSSYAHSQSLDRLMNP
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Last annotation update
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Pred. No. 4.8e-187;
14; Mismatches 50;
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RESULT 8
Q670Q8 9VIRU
ID Q670Q8 9VIRU
ID Q670Q8 9VIRU
AC Q670Q8 9VIRU
DT 25-CCT-2004 (1)
DT 25-CCT-2004 (1)
DT 25-CCT-2004 (1)
DE Capsid protein
GN Namescap;
OS Adeno-associat
OC Viruses; ssDNM
OX NCBL-TaxID=277
RN NUCLEOTIDE SEC
RA Chen C-L., Jer
RA CHEN C-L., Je
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SMR; Q670Q8; 217-735.
SMR; Q670Q8; 217-735.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:005198, F:structural molecule activity; IEA.
GO; GO:005198, P:structural molecule activity; Parvo_coat; 1.
Pfam; pF00740; Parvo_coat; 1.
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Viruses; ssDNA viruses;
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                                                                                                                                                                    NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDN
                                                                                                                                                                                                                                                                  LIDQYLYYLNKTQSASGTVQQSRLLFSQAGPTSMSLQAKNWLPGPCYRQQRLSKQANENN
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                                         VMITDEEEKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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Query Match
Best Local Similarity
Matches 506; Conserv
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tissues.";
J. Virol. 78:6381-6388(2004).
EMBL; AY530591; AAS99276.1; -; Genomic_DNA.
SMR; Q6UC28; 217-735.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0005198; F:structural molecule activity; IE
InterPro; IPRO01403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 735 AA; 81897 MW; 197066F8911FAE9B CR
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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                                                                                                                                                                                                            NIQVKEVTTUDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG
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                                                                                                                      LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKWWLPGPCYRQQRVSKTKTDNN
                                                                                                                                                          YLTLNNGSQAVGRSPFYCLEYFPSQMLRTGNNFQFSYTFEDVPFHSSYAHSQSLDRLMNP
                                                                                                                                                                          YLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLANP
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Pred. No. 2.5
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Q6JC34;
Q5JC34;
Q5JC32004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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EMBL; AY530585; AAS99270.1; -; Genomic_DNA.

SMR; O65034; 217-725.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:005198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat; 1.

SEQUENCE 735 AA; 81962 MW; 85DC69C55232D983
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PubMed=15163731; DOI=10.1128/JVI.78.
Gao G., Vandenberghe L.H., Alvira M.
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.R., Lu Y., Calcedo
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Q6JBZ1 9VIRU

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J. Virol. 78:6381-6388(2004).
EMBL, AY530628; AAS99313.1; -; Genomic_DNA.
SMR; O6JBZ1; 217-735.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity;
GO; GO:0005198; F:structural molecule activity;
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 735 AA; 81868 MW; 1654ED66287F5474 CRC64;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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                      VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
                                                                                                                    NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDN
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Pred. No. 4.1e-
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Matches 505; Conserv
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EMBL; AY530622; AAS99307.1; -; Genomic_D
SMR; Q6JEBZ7; 217-735.

GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule ac
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo coat; 1.

SEQUENCE 735 AA; 81947 MW; EBA318E90
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NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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                                                                                   NIQVKEVTTUDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG
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VMITDEEEIRTINPVATEQYGTVSNNIQNSNTGPTTGTVNHQGALPGMVWQDRDVYLQGP
                           VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
                                                                                                                                                                           LVDQYLYYLNKTQTNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGPCYRQQRLSKQANDNN
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84.3%; Pred. No. 4.1e-186;
tive 41; Mismatches 52;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity;
InterPro; IPR001403; Parvo coat.
Pfam; PF00740; Parvo coat; 1.
SEQUENCE 736 AA; 81660 MW; AFF1EF47B5C67A10
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Q65311;
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Muramatsu S., Mizukami H., Young N.S., Brown K.E.;
"Nucleotide sequencing and generation of an infectious cassociated virus 3.";
virology 221:208-217(1996).
EMBL; U48704; AAC55049.1; -; Genomic_DNA.
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          NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQG
                                                            NNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD
                                                                                              LIDQYLYYLNRTQGTTSGTTNQSRLLFSQAGFQSMSLQARNWLFGFCYRQQRLSKTANDN
                                                                                                          YLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYTFEDVPFHSSYAHSQSLDRLMNP
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 NVMITDEEEIRTTNPVATEQYGTVANNLQSSNTAPTTGTVNHQGALPGMVWQDRDVYLQG
                                              NNSNFPWTAASKYHLNGRDSLVNPGPAMASHKDDEEKFFPMHGNLTFGKEGTTASNAELD
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Pred. No. 7
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Q5JC17;
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O5-JUL-2004 (TrEMBLrel. 2
O5-JUL-2004 (TrEMBLrel. 2
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Wilson J.
"Clades o
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J. Virol. 78:6381-6388(2004).

BMBL; AY530602; AAS99287.1; -; Genomic_DNA.

SMR; Q6JC17; 217-735.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:005198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat. 1.
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
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Viruses; ssDNA viruses;
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84.3%; Pred. No. 2e-1
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"Clades of Adeno-associated viruses are widely tissues.";
J. Virol. 78:6381-6388(2004).
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InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 735 AA; 81913 MW; 51
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PubMed=15.63731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15.63731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo Wilson J.M.;
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EMBL; AY530581; AAS99266.1; -;
SMR; Q6JC38; 217-735.
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Search completed: November 23, 2005, 17:41:18 Job time : 117.377 secs	677 QVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 735	541 QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 599	617 IWAKIPHTDGHFHPSPLMGGFGLKHPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTG 676	481 IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPABFSATKFASFITQYSTG 540



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  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| Cgn2-6/ptodata/1/iaa/BE_COMB.pep:*
| Cgn2-6/ptodata/1/iaa/backfiles1.pep:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd.
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  DB
 US-09-807-802A-15
US-09-807-802A-3
US-09-807-802A-1
US-09-807-802A-17
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US-10-293-478-1
US-10-293-478-1
US-10-038-972A-13
US-10-038-972A-14
US-10-038-972A-15
US-09-532-594B-4
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US-09-533-427-5
US-09-533-427-6
US-09-68-68-68-1
US-08-856-841-120
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APPLICANT: Xiao, Weidong

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Vectors and Host Cells Containing Same

FILE REFERENCE: GNVPN.031USA

CURRENT APPLICATION NUMBER: US/09/807,802A

CURRENT FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR APPLICATION NUMBER: PCT/US99/25694

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 736

TYPE: PRT

ORGANISM: AAV-1
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NSNFTWTGASKYNLNGRESIINPGTAMASHKDDBDKFFPMSGVMIFGKESAGASNTALDN
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                                                                                      LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
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US-09-807-802A-13
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SOFTWARE: PatentIn version
SEQ ID NO 13
LENGTH: 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid TITLE OF INVENTION: Vectors and Host Cells Containing Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wilson, James ! APPLICANT: Xiao, Weidong
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ORGANISM: AAV-1
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  VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
                                                                                                                                                                                                                               LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLFGFCYRQQRVSKTKTDNN 360
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                                                                                         NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDN
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GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR TILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
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; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-17
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Matches 534; Conserv
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IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                                                                 BEBIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
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                                                                       PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                 PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPABFSATKFASFITQYSTGQVSVE
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APPLICANT: PATEL, SALIL D.
APPLICANT: MCARTHUR, JAMES G.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CAI
FILE REFERENCE: 39672
CURRENT APPLICATION NUMBER: US/09/321,589
CURRENT FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 735
TYPE: PRT
ORGANISM: Adeno-associated virus
US-09-321-589-1
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US-09-321-589-1
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Best Local Similarity
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                                              IWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTG 676
                                                             IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
                                                                                                VMITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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QVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
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82.8%; Pred. No. 3.3e
Live 43; Mismatches
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.3e-237;
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RESULT 6 US-10-293-478-1

Sequence 1, Application Patent No. 6733757 GENERAL INFORMATION:

US/10293478

APPLICANT: PATEL,

SALIL

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; APPLICANT: MCARTHUR, JAMES G.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CAI
; FILE REFERENCE: 39672
; CURRENT APPLICATION NUMBER: US/10/293,478
; CURRENT FILING DATE: 202-11-14
; PRIOR APPLICATION NUMBER: US/09/321,589
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PATENTIN VET: 2.1
; SEQ ID NO 1
; SEQ ID NO 1
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US-10-038-972A-13
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                                                                                                                             Sequence 13, Application Patent No. 6962815
GENERAL INFORMATION:
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Best Local (
        APPLICANT: J. BATTlett
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS:
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TYPE: PRT
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Pred. No. 3.36
                                                                                                   AND METHODS
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US-10-038-972A-14

TYPE: PRT ORGANISM: adeno-associated

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Query Match

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SOFTWARE: PatentIn version SEQ ID NO 14

LENGTH: 598

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APPLICANT: J. Bartlett
TITLE OF INVENTION: SAV VECTORS AND METHODS
FILE REFERENCE: 2835/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-0.05
NUMBER OF SEQ ID NOS: 18
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US-10-038-972A-14
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SEQ ID NO 13
LENGTH: 735
TYPE: PRT
ORGANISM: adeno-associated
                                                                                                                                Sequence 14, Applica Patent No. 6962815 GENERAL INFORMATION:
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82.8%;
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Pred. No. 3.36
                                                                                                   AND METHODS
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1.3e-237;
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Sequence 15, Application US/10038972A
Patent No. 6962815
GENERAL INFORMATION:
APPLICANT: J. BARTLETT
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 533
TYPE: PRT
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US-10-038-972A-15
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                                                                                    Query Match
Best Local
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                                       MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
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                                                                         Score 2481.5; DB 2;
Pred. No. 3.2e-212;
Pred. Mismatches 51;
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US-09-532-594B-16
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IEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
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APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
SEQ ID NO 16
LENGTH: 598 OTHER INFORMATION: Description of Artificial OTHER INFORMATION: synthetic construct NAME/KEY: misc_feature OTHER INFORMATION: AAV4 capsid protein VP2 US-09-532-594B-16 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: YKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKL 179 MSDDSEMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGHVTTTSTRTWVLPTYNNHL AVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHL TAPGKKRPLIESPOOPDSSTGIGKKGKOPAKKKLVFEDETGAGDGPPEGSTSG-----A TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNF-GQTGDSESVPDPQPLGEPPATPA 59 YKRLGE----SLQSNTYNGFSTPWGYFDFNRFHCHFSPRDWQRLINNNWGMRPKAMRVKI 56.3%; US/09532594B 74; Score 1830.5; DB 2; Pred. No. 3.7e-154; '4; Mismatches 154; Sequence; Indels Length No. 598; 6468524e 31;

Gaps

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APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
FILE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION UMMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 734
TYPE: PRT
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US-09-532-594B-4
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Best Local Sim
Matches 355;
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APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
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                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e OTHER INFORMATION: synthetic construct NAME/KBY: misc feature
OTHER INFORMATION: AAV4 capsid protein VP1
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YKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKL 179
                                                                              AVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHL 119
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                                                                                                                          TAPGKKRPLIESPQQPDSSTGIGKKGKQPAKKKLVFEDETGAGDGPPEGSTSG-----A
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                         56.3%; Score 1830.5; DB 2; 57.8%; Pred. No. 5.2e-154; ative 74; Mismatches 154;
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                                                                                                                                                                                                                                                   Length 734;
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US-09-533-427-5
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CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Appli
Patent No. 685531
                                                                                                                                                                                       Query Match 52.3%; Score 1700.5; DB 2; Best Local Similarity 55.0%; Pred. No. 1.4e-142; Matches 332; Conservative 64; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
TITLE OF INVENTION: AAVS VECTOR FOR TRANSDUCING
FILE REFERENCE: 14014.0323U2
                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQY 239
                                             GPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALFTYNNHLYK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09533427
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                                                                                                                                              PGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPA-AV
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                     GADTMSAGGGGPLGDNNQGADGVGNASGDWHCDSTWMGDRVVTKSTRTWVLPSYNNHQYR
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                                                                                                                                                                                                                                                                                            Description of Artificial Sequence:/No.synthetic construct
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BRAIN

CELLS

AND LUNG

CELLS

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DAEAGPSGSQQLQIPAQPASSL

52

61

Indels Length

35;

Gaps

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GENERAL INFORMATION:

APPLICANT: Chiorini, John

APPLICANT: Chiorini, Robert M.

APPLICANT: Safer, Brian

APPLICANT: Safer, Brian

APPLICANT: Zaber, Joseph

TITLE OF INVENTION: AAV5 VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELL

FILE REFERENCE: 14014.0323U2

CURRENT APPLICATION NUMBER: US/09/533,427

CURRENT FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 724

TYPE: PRT

OCIGANISM: Artificial Sequence

FEATURE:

FEATURE:

FOTHER INFORMATION: Description of Artificial Sequence:/No. 6855314e =

OTHER INFORMATION: synthetic construct
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                                                                                                                                                         Query Match
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                                                                                         PGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPA-AV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLVDQYLYRFVSTNNTGGVQFNKNL-----AGRYANTYKNWFPGPMGRTQGWNLGSGV
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GPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYK 121
                                                               PKRKKARTEEDSKPSTSS-------DAEAGPSGSQQLQIPAQPASSL
                                                                                                                            Conservative
                                                                                                                                           52.3%;
55.0%;
                                                                                                                           Score 1700.5; DB 2;
Pred. No. 1.9e-142;
4; Mismatches 173;
                                                                                                                              Indels
                                                                                                                                                          Length
                                                                                                                              35;
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APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-532-594B-18
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                                                                                                                                                                           US-09-532-594B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Applicate Patent No. 6468524
GENERAL INFORMATION:
                                                                                                      Matches
                                                                                                                                       Query Match
                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: synthetic construct NAME/KEY: misc feature OTHER INFORMATION: AAV4 capsid protein VP3
                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                      52.0%; Score 1690.5; DB 2.
Local Similarity 59.4%; Pred. No. 9.6e-142;
hes 325; Conservative 65; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
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   127 STGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKE 186
                                                         67 ASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISSA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQVKEVTVQDSTTTIANNLTSTVQVFTDDDYQLPYVVGNGTEGCLPAFPPQVFTLPQYGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPABFSATKFASFIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLEGNMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQEIVPGSVMMERDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRASVSAFATTNRMELEGASYQVPPQPNGMTNNLQGSNTYALENTMIFNSQPANPGTTAT 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQP-KNMLPGPCYRQQRVSKTKTD
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                                     |: ||| : : :||||||||||||::
|AAAGGAAV-EGGQGADGVGNASGDWHCDSTWSEGHVTTTSTRTWVLPTYNNHLYKRLGE-
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                                                                                                                                         DB 2;
                                                                                                          Indels
                                                                                                                                         Length
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GENERAL INCOMMATION:
APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Bafer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
TITLE OF INVENTION: AAV5 VECTOR FOR TRANSDUCING BRA
FILE REFERENCE: 14014.0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT APPLICATION OF SEQ 100-03-22
NUMBER OF SEQ 1D NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ 1D NO 6
LENGTH: 532
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-533-427-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-533-427-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09533427 Patent No. 6855314
                                                                                                                                                      Query Match
Best Local Similarity
Matches 318; Conserv
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                       ASTGASNDNHYFGYSTFWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 185
                                                                                               MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QYLWGLQSTTTGTTLNAGTATTN---FTKLRPTNFSNFKKNWLPGPSIKQQGFSKTA--N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNTSQQQTDRNAFYCLEYFPSQMLRTGNNFEITYSFEKVPFHSMYAHSQSLDRLMNPLID
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GSVDGSNANAYFGYSTPWGYFDFNRFHSHWSPRDWQRLINNYWGFRPRSLRVKIFNIQVK
                                                                        Conservative
                                                                                                                                                  51.2%; Score 1665; DB 2;
58.9%; Pred. No. 1.7e-139;
%tive 54; Mismatches 154;
                                                                                                                                                                                                                                                                      Sequence:/No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRAIN CELLS
                                                                                                                                                                                       Length 532;
                                                                                                                                                        Indels
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                                                                                                                                                      Gaps
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                 GQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 599
                                                         PIWAKIPETGAHFHPSPAMGGFGLKHPPPMMLIKNTPVPGN-ITSFSDVPVS8FITQYST
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GOVTVEMEWELKKENSKRWNPEIOYTNNYNDPOFVDFAPDSTGEYRTTRPIGTRYLTRPL
                                                                         PIWAKIPHTDGHFHPSPLMGGFGLKNPPPOILIKNTPVPANPPABFSATKFASFITQYST
                                                                                                                    NMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQBIVPGSVMMBRDVYLQG
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Search completed: November Job time: 29.2418 secs 23, 2005, 17:42:48

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	% Query Match	Length	BG	ID	Description
1	2906	100.0	534	ω	Y7	a)
N	2906		599	ω	7116	Aay71168 Adeno-ass
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4.	2906	100.0	736	σ	ABB80232	Abb80232 AAV1 vp1
υ	2906	8	736	7	g)	Abr62762 Adeno ass
Φ	2906	100.0	736	7	ADE76565	Ade76565 Adeno-ass
7	2906	8	736	9	ADV70294	Adv70294 Primate a
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φ	2906	8	736	9	ADZ27012	Adz27012 Adeno-ass
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11	2892		736	ø	ADZ27008	Adz27008 Adeno-ass
12	2892	99.5	737	9	ADZ27086	Adz27086 Adeno-ass
13	2888	•	736	9	ADZ27074	Adz27074 Adeno-ass
14	2885	99.3	736	9	ADZ27007	
15	2884		736	4	AAB59847	
16	2884		736	7	ADE76566	
17	2884		736	9	ADV70293	
18	2884		736	9	ADZ27070	Adz27070 Adeno-ass
19	2883		737	9	ADZ27010	Adz27010 Adeno-ass
20	2863	98.5	736	φ	ADZ27009	
21	53		735	9	ADZ26993	Adz26993 Adeno-ass
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Adz27006 Adeno-ass	5 9 ADZ27006	735	86.3	2506.5	<u>4</u> 5
Adz27037 Adeno-ass		734		2511	44
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		735	86.6	2515.5	41
Adz27036 Adeno-ass		734	86.6	2517	40
	5 9 ADZ27004	735	86.7	2520.5	39
_	9	735	86.7	2520.5	38
		735	86.8	2522.5	37
_	5 9 ADZ26998	735	86.9	2524.5	36
_	5 9 ADZ27003	735	86.9	2524.5	35
Adz26992 Adeno-ass	5 9 ADZ26992	735	87.0	2527.5	34
_	5 9 ADZ27067	736	87.0	2528	33
•	5 9 ADV67507	736	87.0	2528	32
Adenc	5 7 ADE76572	736	87.0	2528	31
-	5 7 ABR62763	736	87.0	2528	30
_	5 6 ABB80233	736	87.0	2528	29
AAVJ	6 4 AAB59845	736	•	2528	28
Adenc	5 9 ADZ27000	735	٠	2529.5	27
	5 9 ADZ27076	735	87.0	2529.5	26
	5 9 ADZZ7001	735	87.0	2529.5	25

ALIGNMENTS

RESULT 1 AAY71169 Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy; vaccine; transgene; VP3. 08-SEP-2000 (first entry) AAY71169 standard; protein; 534 AA. 05-NOV-1998; 02-NOV-1999; WO200028061-A2 Adeno-associated virus 1. Adeno-associated virus serotype 1 capsid protein VP3 AAY71169; 18-MAY-2000. (UYPE-) UNIV PENNSYLVANIA. 98US-0107114P 99WO-US025694.

Wilson JM, Xiao W;

N-PSDB; AAD00772, AAD00779. WPI; 2000-376571/32

Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.

Claim 7; Page 99-101; 108pp; English.

The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of services. of a

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RRESULT 2
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Best Local Similarity 100
Matches 534; Conservative
                                                                                                                                                                                                                                                                                                                                                       Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy;
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                                                                                                                                                                                                                                                                                                                               vaccine; transgene;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno-associated virus serotype 1 capsid protein VP2.
                                                                            05-NOV-1998;
                                                                                                                            02-NOV-1999;
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RESULT 3
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                                                                                                                                                                                                                                                                                       LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
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EBBIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
                                                                                                                                                                                                                      WTGASKYNINGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      599 AA;
                                                                                  PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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                                                               PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                                                                                                 EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
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Pred. No. 9.4e-236;
D; Mismatches 0;
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AAY71167 AAY71167;

standard; protein;

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(first entry)

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Best Local S
Matches 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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N-PSDB; AAD00772, AAD00777
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                                                                                                                                                                                          EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN 180
                                                                                                                                                                                                                                                     ASTGASNDNHYFGYSTÞWGYFÐFNRFHCHFSPRDWQRLINNNWGFRÞKRLNFKLFNIQVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 87-90; 108pp; English.
                                                                                                                      NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFBEVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                                                                     ASTGASNONHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 322
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   WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD 360
                                                  LYYLNRTQNQSGSAQNKDLLFSBGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                   NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
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                                  LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
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Pred. No. 1.3e-235;
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Matches 534
                                                                                                                                                                                           The sequences given in ABB80231-34 represent vpl proteins derived from various adeno-associated virus (AAV) serotypes. These sequences were used in the scope of the invention for comparison with the cap protein derived from AAV serotype 9. The AAV capsid comprises three proteins vpl, vp2 and vp3, which are alternative splice variants. The AAV or the nucleic acid molecule is useful for preparing a medicament for delivering a transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adeno-associated virus; splice variant; transger
                                                                                                                                                                                                                                                                                                             New isolated adeno-associated virus (AAV) comprising an AAV9 capsid, useful for preparing a medicament for delivering a transgene to a ce
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05-JUN-2002;
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                                                                                                                  Similarity
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                ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 120
                                                  MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
                                                               MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
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 ASTGASNONHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                                                                                                   100.0%; Score 2906; DB 6; ilarity 100.0%; Pred. No. 1.3e-235; Conservative 0; Mismatches 0;
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2002US-0386132P
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The present sequence is the protein sequence of the vpl capsid protein adeno associated virus serotype 1 (AAV1). The invention provides the nucleic acid and amino acid sequences of novel AAV8 and fragments of these sequences. Each of these fragments may be used in a variety of vector systems and host cella. Among the desirable fragments are the caproteins, including vpl, vp2, vp3 and hypervariable regions, the repproteins, including rep78, rep58, rep52 and rep40, and the sequences encoding these proteins. The fragments may be used alone, in combination
                                                                                                                                                     New adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence of AAV8, useful for preparing a medicament for delivery of a transgene to a cell and for treating cystic fibrosis or hemophilia B.
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01-MAY-2002; 2002US-0377133P
05-JUN-2002; 2002US-0386122P
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ADE76565 standard; protein;

29-JAN-2004 (first entry

Adeno-associated virus (AAV) related protein, SEQ ij Š

hyperproliferative; cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes; antiarthritic; neuroprotective; antidiabetic; antithyroid; dermatological; antiinflammatory; gene therapy; vaccine; adeno-associated virus; AAV; cytostatic; antipsoriatic; antirheumatic;

EP1310571-A2

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01-MAY-2002;
05-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for detecting adeno-associvirus (AAV) sequences in a sample, which comprises subjecting a sacontaining a DNA to amplification via a polymerase chain reaction The AAV sequence have the following activities: cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via
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17-DEC-2001;
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2001US-0341117P.
2002US-0377066P.
2002US-03B6675P.
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No. 1.3e-235;
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                                   cc virion. Also described are; a polynucleotide encoding the mutated protein above; a recombinant AAV virion comprising the mutated protein above; and celivering a recombinant AAV virion to a cell or tissue of a vertebrate subject. The recombinant AAV virion is useful for delivering a celivering a celivering a celivering and celivering celivering celivery to the protein may comparise a non-primate, mammalian celivering celivery to the virion as compared to immunoreactivity of primate celivery, and the heterologous nucleic acid molecule, where the heterologous celivery, and the heterologous nucleic acid molecule, where the heterologous celivery, and the control elements capable of directing the in vivo transcription celivers and celivering and celivering and celivering celivery celiver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutated adeno-associated virus in an AAV virion imparts decreased compared to the corresponding wild-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis; thrombosis; embolism; Parkinson congestive heart failure; cancer; inflammation; muscular dystrophy; diabetes; VP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein that when pu
immunoreactivity to
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30-APR-2004; 2004US-0567310P
03-JUN-2004; 2004US-0576501P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crigler-Najjar syndrome; Gout;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arbetman AE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVIGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       essive; gene therapy; immunogenicity; virus inacti
Pepck deficiency; galactosemia; phenylketonuria;
jar syndrome; Gout; Zellweger syndrome; ischemia;
osis; thrombosis; embolism; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      describes a mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present in an AAV virion imparts decreased protein to the virion as compared to the corresponding wild-type to the virion as compared to the mutated protein above; and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus (AAV) capsid protein that when present eased immunoreactivity to the virion as wild-type virion, useful for treating e.g.
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                                                                                                                                                                        rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative collitis; antirheumatic; antirathritic; neuroprotective; antiinflammatory; antidiabetic; antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological.
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                                                                                                                                                                                                                                                             Adeno-associated virus protein SEQ
                                    30-SEP-2003;
29-APR-2004;
                                                                                                14-APR-2005
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                                                                                                                                                  Adeno-associated
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ilarity 100.0%;
Conservative 0
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2004US-0566546P
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Pred. No. 1.3e-235;
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New adeno-associated virus (AAV) clade comprising at least three members, useful for preventing and/or treating arthritis, multipsclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, base
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                                                                                                                                                   Gao
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                                                                                                                                                   Vandenberghe
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The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.

Sequence 736 Ä

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Matches
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Similarity 100.0%;
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                     IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
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                                                                   PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVB
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Pred. No. 1.3e-235;
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RESULT 9
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AC ADZ2
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30-JUN-2005 ADZ27012;

(first entry)

ADZ27012

protein;

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                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-2003; 2003US-0508226P.
29-APR-2004; 2004US-0566546P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarthritic; neuroprotective; antiinflammatory; antidiabetic;
antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
virucide; antibacterial; cytostatic; antiulcer; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; bacterial infection; cancer; ulcerative colitis; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-2004; 2004WO-US028817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colitis. The present sequence represents adeno-associated virus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 162; 569pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                           MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
                                                                                                                                                                                                                                                        ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKKLNFKLFNIQVK
                                                                                                                                                                                      EVTTNDGYTTIANNLTSTVQVFSDSEYQLFYVLGSAHQGCLFPFFAADVFMIFQYGYLTLN
                                                                                                                                                                                                                                   ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                                                                                                                                                                                                                                                                                                     WASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
                                                                                                                                                                                                                                                                                                                                                                                                                                     736 AA;
   WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD
                                                   LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                    NGSOAVGRSSFYCLEYFPSOMLRTGNNFTFSYTFEEVPFHSSYAHSOSLDRLMNPLIDOY
                                                                                                                     NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                    EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN
                                    LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   Score 2906; DB 9;
Pred. No. 1.3e-235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vandenberghe LH;
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 736;
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Query Match Best Local S Matches 533

Similarity

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Score 2902; DB y; ...; Pred. No. 2.8e-235;

Length; ; Indels

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levels in a subject. The method comprises delivering to the subject a recombinant adeno-associated virus (AAV) comprising a gene encoding a human apolipoprotein E (apoE) or apoA under the control of a regulatory control sequence which directs expression of the gene. The recombinant AAV also comprises a capsid protein selected from an AAV serotype (e.g. AAV) or AAVB) which preferentially expresses high levels of transgene in live. A therapeutically effective amount of apoE or apoA expression is obtained upon delivery of low dose of AAV. The method of the invention is useful for lowering total cholesterol levels in a subject, e.g. for treating atherosclerosis, and for correcting defects in lipoprotein. The present sequence represents a capsid protein of AAV serotype 1 (AAVI), which may be used in recombinant AAV vectors of the invention.
                                                                                                                                                                                                                                                                                          Lowering total cholesterol levels and treating atherosclerosis in subject comprises delivering a recombinant adeno-associated virus comprising an ANV servetype capsid protein or a gene encoding human apolipoprotein E (apoE) or apoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; antilipemic; generapolipoprotein E; apoE; apolipoprotein lipoprotein defect; capsid protein.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-031700/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2003; 2003US-0465293P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adeno-associated virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                               specification describes a method for lowering total cholesterol els in a subject. The method comprises delivering to the subject
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cein A; apoA; a
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New adeno-associated virus (AAV) clade comprising at least three A members, useful for preventing and/or treating arthritis, multiple
                                                                                                                                                                                                                                    30-SEP-2003; 2003US-0508226P
29-APR-2004; 2004US-0566546P
                                                                                                                                                                                                                                                                                                                  30-SEP-2004;
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sclerosis, diabetes,
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                              scleroderma,
569pp;
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                              psoriasis,
                               hemophilia,
                               HΙV,
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The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, ascoridosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.

Sequence 736 A,

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Adeno-associated virus

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rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; bacterial infection; cancer; ulcerative colitis; antirheumatic;

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antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
virucide; antibacterial; cytostatic; antiulcer; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
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29-APR-2004; 2004US-0566546P
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antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV,
virucide; antibacterial; cytostatic; antiulcer; dermatological.
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 IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                           PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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                                           PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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Pred. No. 7.5e-234;
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AAB59847
ID AAB59
XX AAB59
XX AAB59
XX AAB59
XX AAV6
DT 28-MA
XX AAV6
                                                                                AAV6; gene therapy; AAV viral vector; cystic fibrosis; atherosclerosis; sickle cell anaemia; thalassaemia; blood clotting disorder; diabetes; capsid protein VP1.
                                                                                                                                                                                                                                                                                                 AAB59847
                                                                                                                                                                     AAV6 capsid
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                                         Adeno associated virus
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AIDS;

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Best Local Similarity
Matches 529; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adeno-associated virus serotype 6 and viral vector derived from it gene therapy of cystic fibrosis, cancer, acquired immunodeficiency syndrome, sickle cell anemia, thalassemia and diabetes.
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              IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 534
                                                       PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
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99.1%;
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Pred. No. 9.1e-234;
3; Mismatches 2;
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Search

completed: November 23,

2005, 17:35:14

Job time : 97.4286 secs



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16.8
  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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coat protein VP1 -
coat protein 
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C; Superfamily: adeno-assu C; Keywords: coat protein

A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-504 <SRI>
A;Residues: 1-504 <SRI>
A;Cross-references: UNIPROT:P03135; UNIPARC:UPI0000127C8E; EMBL:J01901; NID:g209616; PID
C;Superfamily: adeno-associated virus coat protein

Length

504;

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104	104	104	104.5	104.5	105	05.5	106	06.5	107	107	07.5	.07.5	108	108	108	
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_	hypothetical prote	MAF1 protein - yea	DEF (CLA1) protein	transcription fact	position-specific	hypothetical prote	hypothetical prote	acyl-CoA dehydroge	MAP kinase kinase	probable exported	whn protein - rat	hypothetical prote	penicillin-binding	outer Layer proces	cyclomaltodextrin	

ALIGNMENTS

RESULT 1 VCPV3A

coat protein - adeno-associated virus type 2
C;Species: adeno-associated virus type 2
C;Species: adeno-associated virus type 2
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul
C;Accession: A03698
R;Srivastava, A.; Lusby, E.W.; Berns, K.I.
J. Virol. 45, 555-564, 1983
A;Title: Nucleotide sequence and organization of the adeno-associated A;Reference number: A03694; MUID:83164299; PMID:6300419
A;Accession: A03698

#text_change 09-Jul-2004

δ 밁 Ś Ş 밁 Ś 뭉 ş 밁 Ś 밁 Ś 뫄 맑 Query Match Best Local S Matches 392 ; Local Sim 120 421 301 240 180 181 121 358 361 300 241 61 61 Similarity QS-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK WASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQY NGSQAVGRSSFYCLEYFDSQMLRTGNNFTFSYTFBEVPFHSSYAHSQSLDRLMNPLIDQY EVTQNDGTTT1ANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLN EVTTNDGVTTIANNLTSTVQVESDSEVQLPYVLGSAHQGCLPPEPADVEMIPQYGYLTLN 180 MATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNHLYKQISS EBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQGPIWAKI WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD LYYLSRINTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYS PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPABFSATKFASFITQYSTG EEEIGTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKI WTGATKYHLNGRDSLVNP--AMASHKDDEEKFFPQSGVLIFGKQGSEKTNVNIEKVMITD Conservative 74.9%; 33; Score 2177.5; DB 1; Pred. No. 1.4e-152; 3; Mismatches 47; Indels <u>،</u> Gaps 475 357 240 119 420 360 300 239 179 120 60 60 299

probable phosphoes uncharacterized pr probable periplasm hypothetical prote delta endotoxin -

probable transketo

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418

PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTG

472

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N; Alternate names: V
C; Species: muscovy c
C; Date: 19-Mar-1997
C; Accession: S52210
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A;Residues: 1-732 <ZAD>
A;Residues: 1-732 <ZAD>
A;Cross-references: UNIPROT:Q83289; UNIPARC:UPI00000F6C5D; EMBL:X75093; NID:g609091;
A;Experimental source: strain FM
coat protein VP1 - bovine parvovirus
N;Contains: coat protein VP2
C;Species: bovine parvovirus
                                          RESULT
VCPVB5
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;Alternate names: VP1 protein
;Species: muscovy duck parvovirus
;Date: 19-Mar_1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
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Best Local
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                                                                                                                                                                                                                                           GPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPABFSATKFASFITQYS
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                                                                                                                                                                                                                                                                                                                                                                                                DOYLWNFSEV-NGGRNAO----FKKAVKGAFGAMGRNWLPGPKLLDQRVRAYSGGTDNY
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                         R;Shade, R.O.; Blundell, M.C.; Cotmore, S.F.; Tattersall, P.; Astell, C.R. J. Virol. 58, 921-936, 1986
A,Title: Nucleotide sequence and genome organization of human parvovirus B19 isolated A;Reference number: A24299; MUID:86200451; PMID:3701931
A;Accession: A24299
                                                                                                  C;Species: parvovirus B19
A;Note: host Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision
C;Accession: A24299
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 A; Molecule type: DNA
A; Residues: 1-781 <SHA>
                                                                                                                                                            coat protein VP1 - parvovirus B19
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28-Dec-1987 #text_change

09-Jul-2004

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C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 0
C;Accession: A26104
R;Chen, K.C.; Shull, B.C.; Moses, E.A.; Lederman, M.; Stout, E.R.
J, Virol. 60, 1085-1097, 1986
A;Title: Complete nucleotide sequence and genome organization of
A;Reference number: A26104; MUID:87061184; PMID:3783814
A;Accession: A26104
A;Molecule type: DNA
A;Residues: 1-673 <CHB>
A;Cross-references: UNIPROT:P07297; UNIPARC:UPI0000127D77; EMBL:M
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
C;Keywords: coat protein VP2 #status predicted <VP2>
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                                                                                                                                                                MGGFGLKNPPPQILIK--NTPVPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENS 490
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                                                                                                                                                                                                                            HTFTREARTKLITGSNGADGDYKEWWMLPNQWWDSAPISRYNPIWVKVPRVNRKTLLDTQ
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KNWRPEYMHS---ATNMSVDAYTINNAGVY
                                                  KRWNPEVQYTSNYAKSANVD-FTVDNNGLY
                                                                                                              DGSIPMSHPPGTIFIKLARIPVPGNGD-----
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Pred. No. 4.4e-30;
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A;Cross-references: UNIPROT:P07299; UNIPARC:UPI0000127D7C; EMBL:M13178; NID:g333375; PID C;Superfamily: parvovirus coat protein C;Keywords: coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                            coat protein VPI - porcine parvovirus
N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09
C;Accession: B3302
R;Ranz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A;Title: Porcine parvovirus: DNA sequence and genome organization.
A;Reference number: A33302; MUID:90010964; PMID:2794971
A;Accession: B33302
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A;Residues: 1-723 <RAN>
A;Cross-references: UNIPROT:P18546; UNIPARC:UPI0000174964;
C;Genetics:
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Matches 139
                                                                                                                                                                                                                Superfamily: parvovirus coat protein;
Keywords: coat protein;
145-723/Product: coat protein VP2 #s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAGASNTALDNV-----MITDEEEIKATNPVATERFGTVAVNFOSSSTDPATGDVHAM
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SGGGGG-GGGGRGAGGVGVSTGSFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKR
                                                SGGGAPMADNNEGADGVGNASGNWH--CDSTWLGD---RVITTSTRTWALPTYNNHLYKQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAEFSATKFASFITQYSTGQVSVEIEWEL-QKENSKRWNPE 496
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                                                                                                         8.1%; Score 234.5; DB 1; 23.2%; Pred. No. 3.2e-09; tive 83; Mismatches 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
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Pred. No. 8.3e-28;
4: Mismatches 239;
                                                                                                                                                                                                                      <VP2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coat protein VP1 - porcine parvovirus (strain 90HS)

N;Contains: coat protein VP2

C;Species: porcine parvovirus

C;Date: 30.-Sep-1993 #sequence_revision 30.-Sep-1993 #text_change

C;Accession: A60006

C;Accession: A60006

C;Accession: N; Nishimori, T.; Ushimi, C.; Nakajima, H.

Virus Res. 13, 79-86, 1989

A;Title: Nucleotide sequence of capsid protein gene of porcine p

A;Reference number: A60006; MUID:89319168; PMID:2750278

A;Accession: A60006

A;Molecule type: DNA

A;Ressidues: 1-729 <SAK>
A;Recession: NINIBARC: INIBARC: INI
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                                                      112 FKLFNIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADV
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     QEIFNVVLKTITESATSPPTKIYNNDLTASLMVALDTNNTLPYTPAAPRSETLGFYPWLP
                                                                                                               IHVLNSESGVAGQMVQDDAHTQMVTPWSLIDANAWGVWPNPADWQLISNNMTEINLVSFE
                                                                                                                                                                                                                         SGGGGG-GGGGRGAGGVGVSTGSFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKR
                                                                                                                                                                                                                                                                          SGGGAPMADNNEGADGYGNASGNWH---CDSTWLGD---RVITTSTRTWALPTYNNHLYKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKCGRAPKQQFNQQAPLNLENTNNGTLLPSDPIGGKSNMHFMNTLNTYGPLTALNNTAPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIVPTADTQYNDDEPN-----
                                                                                                                                                                      IS--SASTGAS----NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLN
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                             8.0%;
23.0%;
                                                                                                                                                                                                                                                                                                                                      6;
                                                                                                                                                                                                                                                                                                                                   Score 232.5; DB 1
Pred. No. 4.5e-09;
6; Mismatches 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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09-Jul-2004

526 657

706

603 410 543

Gaps

2

57

111

232

168 292 (covalent) #stati

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498 317

369

464 257 406 346 168

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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 11-729 <BER>
A;Cross-references: UNIPARC:UPI0000174965
A;Experimental source: NADL-2, ATCC VR-742
A;Experimental source: NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:138794)
C;Genetics:
A;Introns: 10/1
C;Superiamily: parvovirus coat protein
C;Koywords: coat protein; Glycoprotein
C;Koywords: coat protein VP2 #status predicted <VP2>
F;32,172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn)
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VCPVNA

VCPVNA

COAT protein VP1 - porcine parvovirus (strain N;Contains: coat protein VP2

C;Species: porcine parvovirus

C;Species: porcine parvovirus

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-
C;Accession: B33743; D48472

C;Accession: B33743; D48472

C;Accession: B3743; D48472
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A;Title: Genomic organization and mapping of transcription A;Reference number: A48472; MUID:94025614; PMID:8212598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Nucleotide sequence analysis of the capsid genes A; Reference number: A33743; MUID: 90085785; PMID: 2596019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, Virology 173, 368-377, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Vasudevacharya,
                                                                                                                                                                                 Query Match
Best Local
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                                     58
                                                                                                                                                          Similarity 23.0
38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TFSYTFEEVPFHSSYAHSQSLDR-----LMNPLI--DQYLYYLNRTQNQSGSAQNK 257
  IHVLNSESGVAGQMVQDDAHTQMVTPWSLIDANAWGVWFNPADWQLISNNMTEINLVSFE
                                                                               SGGGGG-GGGGRGAGGVGVSTGTFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKR
                                                                                                                    SGGGAPMADNNEGADGVGNASG--NWHCDSTWLGD---RVITTSTRTWALPTYNNHLYKO
                                   IS--SASTGAS----NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLN
                                                                                                                                                                              8.0%;
23.0%;
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                                                                                                                                                                              Score 232.5; DB 1;
Pred. No. 4.5e-09;
                                                                                                                                                              Mismatches
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(;Species: parvovirus LuIII
(;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text
(;Accession: B44276
R;Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
Virology 192, 339-345, 1993
A;Title: The complete nucleotide sequence of parvovirus
A;Accession: B44276
A;Accession: B44276
A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-587 <DIF>
A;Residues: 1-587 <DIF>
A;Cross-references: UNIPROT: P36310; UNIPARC: UPI0000127D7E; GB:M8188
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein; glycoprotein
C;Keywords: coat protein; glycoprotein
E;49,90,220,304,371,503,511,514,539,571/Binding site: carbohydrate
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                      203
                                                                                                                                                                                   84 VRVHNTNDTGTASHMAMDDAHEQIW-TPWSLVDANAWGVWFQPSDWQYISNNMIHINLHS
                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                  30
                                                                                                                                                                                                                                                                                                     3 SGGGAPMADNNEGADGVGNASGNWHCDS--TWLGD---RVITTSTRTWAL--PTYNN---
                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                    LNFKLFNIQVKEVT-TNDGVTTIA---NNLTSTVQVFSDSEYQLFYVLGSAHQGCL----
                                                                                                                                                                                                                      ---HLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKR
                                                            --PPFPA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKCGRAPKQQFNQQAPLNLENTNNGTLLPSDPIGGKSNMHFMNTLNTYGPLTALNNTAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIVPTADTQYNDDEPN-------GAIRFTMDYQHGHLTTSSQELERYTFNPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P--GTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD---NVMITDEEEIK--ATNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNSYTEAT ----AIRP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIIN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STGIYHFDTKPL--KLTHSWQTNRSLGLPPKLLTEPTTEGDQHPGTLPAANTRKGYHQTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKPTQYRYYLSCIRNLNPPTYTGQSQQITDSIQTGLHSDIMFYTIENAVPIHLLRTGDEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FMIPQYGYL-----TLNNGSQAVGRS-----SFYCLE-YFPSQMLRTGNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKLFNIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADV
                    WKPTIPSPYRYYFSCDRNLSVTYKDEAGTITDTMGLASGLNSQFFTIENTQRINLLRTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPNGQIWDKELDTDLKPRLH----VTAPFVCKNNPPGQLFVKIAP----NLTDDFNADSPQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VATERFGTVA-VNFQSSS-----TDPATG--DVHAMGALP-----GMVWQDRDV
                                                                                                 LDQELFNVVIKTVTEQNTGAEAIKVYNNDLTAAMMVALDSNNILPYTPAIDNQETLGFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TFSYTFEEVPFHSSYAHSQSLDR-----LMNPLI--DQYLYYLNRTQNQSGSAQNK 257
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                              -GSGGGGVGVSTGSYDNQTHYKFLGDGWVEITAYSTRMVHLNMPKSENYCR
                                                                                                                                                                                                                                                                                                                                                             7.9%;
                                                            ---- DVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPS-QMLRTGN 206
                                                                                                                                                                                                                                                                                                                                           74;
                                                                                                                                                                                                                                                                                                                                                               Score 229; DB 1;
Pred. No. 5.9e-09;
                                                                                                                                                                                                                                                                                                                                             Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-Feb-1994 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                  Length 587
                                                                                                                                                                                                                                                                                                                                             Indels 150;
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Qy 265 SPAGMSVQPKWL	GVTTIANNLITSTVQVFSDSEYQLFYVLGSAHQGCLPFFPA	Query Match Best Local Similarity 20.0%; Pred. No. 1.8e-06; Best Local Similarity 20.0%; Pred. No. 1.8e-06; Matches 126; Conservative 88; Mismatches 241; Indels 174; Gaps 28; Matches 126; Conservative 88; Mismatches 241; Indels 174; Gaps 28; Qy 3 SGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQ 57	C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004 C;Accession: A03700 C;Accession: A03700 R;Astell, C.R.; Thomson, M.; Merchlinsky, M.; Ward, D.C. Nucleic Acids Res. 11, 999-1018, 1983 A;Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus. A;Reference number: A03696; MUID:83143341; PMID:6298737 A;Accession: A03700 A;Molecule type: DNA A;Residues: 1-716 <ast> A;Cross-references: UNIPROT:P03137; UNIPARC:UPI0000127D6D; EMBL:V01115 C;Superfamily: parvovirus coat protein C;Keywords: coat protein</ast>		

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C;Species: minute virus of mice (strain MVMi)
C;Species: minute virus of mice, murine parvovirus
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul
C;Accession: B23008; B29510
R;Sahli, R.; McMaster, G.K.; Hirt, B.
Nucleic Acids Res. 13, 3617-3633, 1985
A;Title: DNA sequence comparison between two tissue-specific variants
A;Reference number: A23008; MUID:85242059; PMID:3855242
A;Accession: B23008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P07302; UNIPARC:UPI0000174963; EMBL:X02481; R;Astell, C.R.; Gardiner, E.M.; Tattersall, P. J. Virol. 57, 656-669, 1986
A;Title: DNA sequence of the lymphotropic variant of minute virus of mic
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VCPVIM
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C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
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A; Residues: 1-143,'A',145-718 < AST>
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Best Local Simi
Matches 122;
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   592
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                                    409 DVYLQGPIWAK---IPHTDGHFHPSPLMGGFGLKNPPPQILIKNTP--VPANPPAEFSAT
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                                                                                                                                                                                                                                                              GSPAGMSVQPKNWL-----
                                                                                                                                                                                                                                                                                                                                   NF-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQSGSAQNKDLLFSR 263
                                                                                                                                                                                                                                                                                                                                                                                                            DVFMIPQYGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOEIFNVVLKTVTEQDSGGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFKLFNIQVKEVTTND----GVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGGG-----GSGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGGGAPMADNNEGADGVGNASGNWHCDS--TWLGD---RVITTSTRTWALPTYNNHLYKQ
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PYYPQGQIWDKELDLEHKPRLHITAPFV----CKNNAPGQMLVRLGPNLTDQYDPNGATLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNGLY---TEPRPIGT----RYLTRPL
                                                                                                             TALDNVMITDEEEIKATNPVATERFGTVAVNFQS--SSTDPATGDVHAMGALPGMVWQDR
                                                                                                                                                                                     TWTGASKYNLNGRESIINPGTAMASHKDDEDKF-----FPMSGVMIFGKESAGASN
                                                                                                                                                                                                                        GSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRAGP-FAAPKVPADVTQGVDREA
                                                                                                                                                                                                                                                                                                 EFATGTYYFDTNPV--KLTHTWQTNRQLGQPPLLSTF----PEADTDAGT-----LTAQ
                                                                                                                                                                                                                                                                                                                                                                         KPTIASPYRYYFCVDRDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I-----SSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRL
                                                                                                                                                 NGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILT
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20.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                          -LTLNN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 196.5; DB Pred. No. 2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                            -GSQAVGRSSFYCLEYFPS-QMLRTGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: mink enteritis virus, MEV
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Best Local
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                   TYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN-
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                                                                                                                                                                                                                                                                                                                    RGGAQTDENQAADGDPR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGSAHQGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLIVNTMSELHLVSFEQEIFNVVLKTVSESATQPPTKVYNNDLTASLMVALDSNNTMPFT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRLINNNWGFRPKRLNFKLFNIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGQP-AVRNERATGSGNGSGGGGGGGS--GGVGISTGTFNNQTEFKFLENGWVEITANSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIVTYGTFFWKGKLTMRAKLRA----NTTWNPVYO-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQFYTIENSVPVHLLRTGDEFATGTFFFDCKPCRLTHTWQTNRALGLPPFLNSLPQSEGA 438
                                                       QYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                                FHPSPLMGGFGLK-----
                                                                                                                                                                                                       TNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGH 426
                                                                                                                                                                                                                                                                                 NLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD-NVMITDEEEIKA 366
                                                                                                                                                                                                                                                                                                                                                                                         TNFGDIGVQQDKRRGVTQMGNTDYITEATIMRPAEVGYSAPYYSFEASTQGPFKTPIAAG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SFYCLE-YFPSQMLRTGNNF---TF-----SYTFEE------VPFHSSYAHSQSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAAMRSETLGFYPWKPTIPTPWRYYFQWDRTLIPSH-----TGTSGTPTNIYHGTDPDD 378
                                                                                                                                                                    TDPIG----GKTGINY--TNIFNTYGPLTALNNVP-----PVYPNGQIWDKEFDTD--
                                                                                                                                                                                                                                                                                                                                                      -GSAQNKDLLFSRGSPAGMSVQPKNWLPGPCY---RQQRVSKTKTDNNNSNFTWTGASKY 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PPFPA-----DVFMIPQYGYLTLNNGSQAVGRS-----
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                                                                                           LKPRLHVNAPFVCQNNCPGQLFVKVAPNLTNEYDPDASANMSR----IV
                                                                                                                                                                                                                                             ---IAHQDT-----GRYPAGDWIQNINFNLPVTNDNVLLP
                                                                                                                                                                                                                                                                                                                                                                                                                               -----LMNPLIDQYL--YYLNRTQNQS-----
                                                                                                                                ----NPPPQILIKNTPVPAN---PPAEFSATKFASFIT 470
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                                                                                                                                                                                                                                                                                                                    ----YAFGRQHGQKTTTTGETPERFTY-----
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A; Molecule type: DNA
A; Residues: 1-727 <CAR>
A; Cross-references: UNIPROT: P04864; UNIPARC:
C; Genetics: 1./1
C; Superfamily: parvovirus coat protein
C; Keywords: coat protein
C; Keywords: coat protein
F; 144-727/Product: coat protein VP2 #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Carlson, J.; Rushlow, K.; Maxwell, I.; Maxwell, F.; Win J. Virol. 55, 574-587, 1985
A;Title: Cloning and sequence of DNA encoding structural A;Reference number: A03697; MUID:85265017; PMID:2991581
A;Accession: A03701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Contains: coat protein VP2
C;Species: feline panleukopenia virus,
C;Date: 30-Jun-1987 #sequence_revision
C;Accession: A03701
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Best Local Similarity
Matches 136; Conserv
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   protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRLINNNWGFRPKRLNFKLFNIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLVHLNMPESENYKRVVVNNMDKTAVKGNMALDDTHVQIVTPWSLVDANAWGVWFNPGDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---HL-----YKQI-----SSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
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                                                                                                                                                                                                                                                     TNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQGPIWAKIPHTDGH
                                                                                                                                                                                                                                                                                                                                                                                                                         TNFGDIGVQQDKRRGVTQMGNTDYITEATIMRPAEVGYSAPYYSFEASTQGPFKIPIAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAAMRSETLGFYPWKPTIPTPWRYYFQWDRTLIPSH-----TGTSGTPTNIYHGTDPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGSAHQGCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLIVNTMSELHLVSFEQEIFNVVLKTVSESATQPPTKVYNNDLTASLMVALDSNNTMPFT
                                                                                     TYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN----
                                                                                                                  QYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                                                                                     FHPSPLMGGFGLK-----
                                                                                                                                                                                                                                                                                      -----IAHQDT-
                                                                                                                                                                                                                                                                                                                     NLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD-NVMITDEEEIKA
                                                                                                                                                                                                                                                                                                                                                      RGGAQTDENQAADGDPR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SFYCLE-YFPSQMLRTGNNF---TF----SYTFEE-----VPFHSSYAHSQSL
                                                                                                                                                                                                                                                                                                                                                                                      -GSAQNKDLLFSRGSPAGMSVQPKNWLPGPCY---RQQRVSKTKTDNNNSNFTWTGASKY
     VP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNIPROT: P04864; UNIPARC: UPI0000127D55; EMBL: M10824; NID: g333474;
     canine
                                                                                                                                                                                                                      - GKTGINY - - TNI FNTYGPLTALNNVP - - - - - PVY PNGQIWDKEFDTD - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.7%; Scor. No. 3.11 20.7%; Pred. No. 3.11 --ive 73; Mismatches 215; --ive 73; Mismatches 215;
                                                                                                                                                   - LKPRLHVNAPFVCONNCPGOLFVKVAPNLTNEYDPDASANMSR----
   parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PPFPA-----DVFMIPQYGYLTLNNGSQAVGRS-----
                                                                                                                                                                                     -----NPPPQILIKNTPVPAN----PPAEFSATKFASFIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I.; Maxwell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-Jun-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LMNPLIDQYL--YYLNRTQNQS-----
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                                                                                                                                                                                                                                                                                      -GRYPAGDWIQNINFNLPVTNDNVLLP
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coat protein VP1 - feline panleukopenia virus N;Contains: coat protein VP2 C;Species: feline panleukopenia virus, FPLV C;Date: 31-Dec-1991 #sequence_revision 31-Dec-C;Accession: B36608

R;Martyn, J.C.; Da J. Gen. Virol. 71,

Davidson, B.E.; 71, 2747-2753, 19

1990

Studdert,

31-Dec-1991 М .

#text_change

09-Jul-2004

(strain

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A;Title: Nucleotide sequence of feline panleukopenia virus: A;Reference number: A36608; MUID:91073139; PMID:2174965

comparison

with

canine

parv

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C;Species: canine parvovirus, CPV
C;Date: 05-Mar-1995 #sequence revi
C;Accession: S4594
R;Mizak, B.; Plucienniczak, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, November 1994 A;Description: Polish isolates of canine parvovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: Q66208; UNIPARC: UPI00000FA046; EMBL: Z46651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-584 < MIZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S49594
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Local Similarity 20.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGSAHQGCL
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                            KRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAAMRSETLGFYPWKPTIPTPWRYYFQWDRTLIPSH-----TGTSGTPTNIYHGTDPDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLVHLNMPESENYRRVVVNNLDKTAVNGNMALDDTHAQIVTPWSLVDANAWGVWFNPGDW
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                                                          PFVCQNNCPGQLFVKVAPNLTNEYDPDASANMSR---
                                                                                        ----NPPPQILIKNTPVPAN----PPAEFSATKFASFITQYSTGQVSVEIEWELQKENS
                                                                                                                            IFNTYGPLTALNNVP-----PVYPNGQIWDKEFDTD---
                                                                                                                                                        TDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK-----
                                                                                                                                                                                                                          DEDKFFPMSGVMIFGKESAGASNTALD-NVMITDEEEIKATNPVATERFGTVAVNFQSSS
                                                                                                                                                                                                                                                        TQGPFKTPIAAGRGGAQTDENQAA----DGDPRYAFGRQHGQKTTTTGETPERFTYIAHQD
                                                                                                                                                                                                                                                                                         SK----
                                                                                                                                                                                                                                                                                                                        SEGGTNFGYIGVQQDKRRGVTQMGNTNYITEATIMRPAEVGYS
                                                                                                                                                                                                                                                                                                                                                      TQNQS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSAQNK------DLLFSRGSPAGMSVQPKNWLPGPCYRQQRV
                                                                                                                                                                                                                                                                                        ----TKTDNNNSNFTWTGASKY---NLNGRESIINPGT----AMASHKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coat protein
                                                                                                                                                                                        -GRYPEGDWIQNINFNLPVTDDNVLLPTDPIG----GKTGINY--TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 189; DB 2;
Pred. No. 5.2e-06;
VDNQFNYV-PSNIG
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                               526
567
                                                              - IVTÝSDEWWKGKLVEKAKLRAS
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A;Accession: B36608
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-727 <MAR>
A;Residues: 1-727 <MAR>
A;Cross-references: UNIPROT:P24840; UNIPARC:UPI0000127D56; GB:X55115
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
P;144-727/Product: coat protein VP2 #status predicted <VP2>
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Search completed: November 23, 2005, Job time: 20.8571 secs
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Best Local Similarity
Matches 135; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---HL-----YKQI------SSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
                                                            TYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN---
                                                                                         QYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG 526
                                                                                                                       FHPSPLMGGFGLK------NPPPQILIKNTPVPAN---PPAEFSATKFASFIT
                                                                                                                                                                                   TDPIG----GKTGINY--TNIFNTYGPLTALNNVP---
                                                                                                                                                                                                                INPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGH 426
                                                                                                                                                                                                                                              ------IAHQDT------GRYPEGDWIQNINFNLPVTNDNVLLP
                                                                                                                                                                                                                                                                         NINGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD-NVMITDEEEIKA 366
                                                                                                                                                                                                                                                                                                           RGGAQTDENQAADGDPR-----YAFGRQHGQKTTTTGETPERFTY-----
                                                                                                                                                                                                                                                                                                                                        -GSAQNKDLLFSRGSPAGMSVQPKNWLPGPCY---RQQRVSKTKTDNNNSNFTWTGASKY
                                                                                                                                                                                                                                                                                                                                                                      TNFGDIGVQQDKRRGVTQMGNTDYITEATIMRPAEVGYSAPYYSFEASTQGPFKTPIAAG
                                                                                                                                                                                                                                                                                                                                                                                                    DR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  VQFYTIENSVPVHLLRTGDEFATGTFFFDCKPCRLTHTWQTNRALGLPPFLNSLPQSEGA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAAMRSETLGFYPWKPTIPTPWRYYFQWDRTLIPSH-----TGTSGTPTNVYHGTDPDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTST-----RTWALPTYNN- 52
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20.6%; Pred. No. 7.2e-06;
ative 73; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    -----LMNPLIDQYL--YYLNRTQNQS-----
                 17:44:04
                                                                                                                                                                                   ----PVYPNGQIWDKEFDTD--
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                                                            -- VDNQFNYV-PNNIG
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Title:
Perfect score:
Sequence:
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                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                         Database :
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Maximum DB seq length: 200000000
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2906
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UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

33222222221111111111111111111111111111	Result No.
22 25 25 25 25 25 25 25 25 25 25 25 25 2	Score
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Best Local S
Matches 532
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tissues";
J. Virol. 78:6381-6388(2004).
BMBL; AX530607; AA899292.1; -; Genomic_DNA.
SMR; Q6JC12; 217-736.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IE
InterPro; IPRO01403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 736 AA; 81364 MW; F2D75A06662E6376 CR
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C12 9VIRU
C12 9VIRU PRELIMINARY;
QGUC12;
Q6UC12;
05-UUL-2004 (TrembLrel. 27,
05-UUL-2004 (TrembLrel. 27,
05-UUL-2004 (TrembLrel. 27,
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Can G.. Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
                                                                                                                                                                                  WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD
                                                                                                                                                                                                                                                                                         LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                                                                                                                                                                                                                                                                                     NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                                                                                                                                                                                                                                   NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN
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                                                                                 EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
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PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                   EEEI KATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQGRDVYLQGPI WAKI
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Pred. No. 1.3e-202
0; Mismatches 2
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EMBL; AY530611; AAS99296.1; -; Genomic_DNA.

SMR; Q6JC08; 217-736.

G0; G0:0019028; C:viral capsid; IEA.

G0; G0:0019028; F:structural molecule activity;

InterPro; IRR001403; Parvo_coat.

Pfam: PF00740; Parvo_coat: 1.
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo Wilson J.M.;
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05-JUL-2004 (TrEMBLrel.
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SEQUENCE 736 AA; 81317 MW;
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3; Mismatches 2;
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A Rutledge E.A., Halbert C.L., Russell D.W.;

ART "Infectious clones and vectors derived from adeno-associated virial cancer than AAV type 2.";

RT (AAV) serotypes other than AAV type 2.";

RL J. Virol. 72:309-319(1998).

DR EMBL; AF028704; AAB95450.1; -; Genomic_DNA.

DR SWR; O556137; 217-736.

DR GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

DR Hofam; PF00740; Parvo_coat.

DR Pfam; PF00740; Parvo_coat.

DR Pfam; PF00740; Parvo_coat.

DR Pfam; PF00740; Barvo_coat.

DR Pfam; PF00740; Barvo_coat.

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SMR; Q6JC13; 218-737.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0015198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.
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PubMed=15163731; DOI=10.1128/JVI.78.
Gao G., Vandenberghe L.H., Alvira M.
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Viruses; ssDNA viruses;
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PubMed=15163731; DOI=10.1128/JVI.78.
Gao G., Vandenberghe L.H., Alvira M.
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EMBL; AY530609; AA599294.1; -
SMR; Q6JC10; 217-736.
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Viruses; ssDNA viruses;
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Capsid protein VPl.
Name=cap;
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  Adeno-associated virus
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GO:0005198; F:structural molecule activity;
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RESULT 8
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GO; GO:0019028; C:viral capsid; IE
GO; GO:0005198; F:structural molec
GO; GO:0005198; F:structural molec
InterPro; IPR001403; Parvo coat; I.
SEQUENCE 735 AA; 81962 MW; 85D
                                   Adeno-associated virus.
Viruses; ssDNA viruses;
NCBI TaxID=272636;
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EMBL; AY530585; AAS99270.1; -
SMR; Q6JC34; 217-735.
G0; G0:0019028; C:viral capsi
G0; G0:0005198; F:structural |
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=0G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
Wilson J.M.;
                                                                                                     Capsid protein Name=cap;
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Pred. No. 1.3e-
34; Mismatches
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Best Local Sim:
Matches 455;
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T "Characterization of Adeno-Associated Viruses In Children."
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; AY695376; AAU05370.1; -; Genomic_DNA.

R SMR; Q670Q8; 217-735.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0095198; F:structural molecule activity; IEA.

R GO; GO:0095198; P:structural molecule activity; IEA.

R GO; GO:00740; Parvo_coat.

R Pfam; PF00740; Parvo_coat; 1.

R SEQUENCE 735 AA; 81887 MW; 258BFB955F1C9925 CRC64;
                                                                                                                                                                                                                                                         ULT 9
C28 9VIRU
OGJC28 9VIRU PRELIMINARY;
OGJC28;
O5-JUL-2004 (TrEMBLrel. 2
                                                                   NUCLEOTIDE SEQUENCE.

PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo Wilson J.M.;
                                                                                                                                                         NCBI_TaxID=272636;
[1]
                                                                                                                                                                                                Adeno-associated virus. Viruses; ssDNA viruses;
                      "Clades of Adeno-associated tissues.";
    Virol.
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Best Local S
Matches 454
Gao G., Vandenberghe L.H., Alvira Wilson J.M.;
"Clades of Adeno-associated viruse tissues.";
J. Virol. 78:6381-6388(2004).
EMBL; AY530622; AAS99307.1; -; Gen SMR; OGJBZ7; 217-735.
GO; GO:00101028; C:viral capsid; IE GO; GO:0005198; F:structural molec
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SMR;
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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GO; GO:0015028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecul
GO; GO:0005198; F:structural capsid;
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 735 AA; 81897 MW; 19708
                                                                                                                                                  PubMed-15163731; DOI=10.1128/JVI.78.

PubMed-15163731; DOI=10.1128/JVI.78.
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Best Local
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MEDLINE=98080418; PubMed=9420229;
Rutledge E.A., Halbert C.L., Russell D.W.;
"Infectious clones and vectors derived from adeno-
(AAV) serotypes other than AAV type 2.";
J. Virol. 72:309-319(1998).

EMBL; AP028705; AAB95452.1; -; Genomic_DNA.
SMR; O56139; 217-736.
GO; GO:0005198; F:structural molecule activity; IE
RITHEPPRO; IPR001403; PARVO_COAt.
Query
Best I
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39 9VIRU
056139_9VIRU PRELIMINARY;
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01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                            InterPro; IPRO
Pfam; PF00740;
SEQUENCE 736
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Viruses; ssDNA viruses;
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               BIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                               IPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSV
                                                                                                                        DEEBIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQGPIWAK
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 EIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
                                                    I PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTPVPANPPTTFSPAKFASFITQYSTGQVSV
                                                                                                      DEEEIRTTNPVATEQYGTVANNLOSSNTAPTTRTVNDQGALPGMVWQDRDVYLQGPIWAK
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G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0005198; F:structural molecule InterPro; IPR001403; Parvo_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno-associated virus.
Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                            Pfam; PF00740;
SEOUENCE 735
                                                                                                                                                                                                                                                                                                                                                                               "Clades of Adeno-associated viruses tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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Q6JBZ1;
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Score 2529.5;
Pred. No. 4.2e
34; Mismatches
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Q65311;
01-NOV-1996 (
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EMBL; U49704; AAC55049.1; -; Genomic_DNA.

SMR; Q65311; 217-736.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR001403; Parvo_coat.

Pfam; pF00740; Parvo coat; 1.

SEQUENCE 736 AA; 81660 MW; AFF1EF47B5C67A10 CRC64;
                                                                                                                                                                                                                                                              MEDLINE=96266430; PubMed=8661429; DOI=10.1006/viro.1996.0367; Muramatsu S., Mizukami H., Young N.S., Brown K.E.; "Nucleotide sequencing and generation of an infectious clone associated virus 3.";
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01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Pred. No. 5.5e-176;
8; Mismatches 46;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule InterPro; IPR001403; Parvo coat.
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NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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SEQUENCE 735
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AA; 81913 MW;
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Pred. No. 9.8e-176;
4; Mismatches 46;
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Matches 453;
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Q6C42 9VIRU PRELIMINARY;
Q6C42 9VIRU PRELIMINARY;
Q6JC42;
05-JUL-2004 (Tremblrel. 27,
05-JUL-2004 (Tremblrel. 27,
05-JUL-2004 (Tremblrel. 27,
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EMBL; AYS30577; AAS99262.1; -; Genomic_DNA.

SMR; Q6GC42; 217-725.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:005198; F:structural molecule activity;

InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat; 1.

SEQUENCE 735 AA; 82114 MW; 59E748255744D5FB
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Cao G. Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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                       NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
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 IEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
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Search completed: 1 Job time: 104.857 November secs 23, 2005, 17:41:20

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Total number of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Listing first 45 summaries
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1817.892 Million cell updates/sec
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US-09-807-802A-15
US-09-807-802A-13
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US-10-038-972A-14
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US-10-293-478-1
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US-09-533-427-5
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US-09-533-427-7
US-08-856-841-20
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Sequence 13, Appl
Sequence 14, Appl
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Sequence 14, Appl
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Sequence 18, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 37, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 31, Appl
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APPLICANT: Wilson, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
SOFTMARE: Patentin version 3.1
SEQ ID NOS: 20
SOFTMARE: Patentin version 3.1
TYPE: PRT
ORGANISM: AAV-1
US-09-807-802A-17
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                                                             NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
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US-09-107-532A-3813

US-08-489-202-27

US-08-489-202-27

US-08-484-34C-34

US-09-384-361-34

US-08-384-361-34

US-08-357-688-6

US-08-357-698-6

US-08-359-554A-4

US-08-359-554A-4

US-08-359-554A-4

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Patent No. 523424
Sequence 2, Appli
Sequence 17, Appl
Sequence 4, Appli
Sequence 3855, Ap
Sequence 23413, A
Sequence 24, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 17, Appl
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Sequence 18, Appli
Sequence 28, Appli
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Result No.

Score

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Query

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APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weidong
ITITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid
ITITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid
ITITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 599
TYDE: PRT
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US-09-807-802A-15
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; ORGANISM: AAV-1
US-09-807-802A-15
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Best Local Simi
Matches 534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILLING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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US-09-807-802A-3
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US-09-807-802A-3
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GENERAL INFORMATION:
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Best Local Similarity
Matches 534; Conserv
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TYPE: PRT
ORGANISM: AAV-1
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APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
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Pred. No. 1.6e-257;
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PILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 736
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                                                         RESULT 5
US-10-08-972A-15
; Sequence 15, Application
; Patent No. 6962815
; GENERAL INFORMATION:
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Best Local Similarity
Matches 534; Conserv
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APPLICANT: Wilson, James |
APPLICANT: Xiao, Weidong
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ORGANISM: AAV-1
-09-807-802A-13
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APPLICANT: J. Bartlett
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
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al Similarity 100.0%;
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Pred. No. 1.6e-257;
Mismatches 0;
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    Query Match
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CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VERBION 3.1
SEQ ID NO 15
LENCTH: 533
TYPE: PRT
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US-10-038-972A-14
; LENGTH; 598
TYPE: PRT
; ORGANISM: adeno-associated
US-10-038-972A-14
                                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 14
                                                                                                                                                                                                                                                                            Patent No. 6962815
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/10038972P
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Best Local Similarity
                                                                                                                TITLE OF INVENTION: AAV VECTORS AND METHODS FILE REFERENCE: 28335/36996US CURRENT PPLICATION NUMBER: US/10/038,972A CURRENT FILING DATE: 2002-01-04 PRIOR APPLICATION NUMBER: US 60/260,124 PRIOR PILING DATE: 2001-01-05 NUMBER OF SEQ ID NOS: 18
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83.3%; Pred. No. 8.3e-219;
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Sequence 1. Application US/09321589

| Sequence 1. Application US/09321589 |
| Patent No. 6498244 |
| GENERAL INFORMATION: |
| APPLICANT: PATEL, SAILL D. |
| APPLICANT: PATEL, SAILL D. |
| APPLICANT: WCARTHUR, JAMES G. |
| TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS |
| FILE REFERENCE: 39672 |
| CURRENT APPLICATION NUMBER: US/09/321,589 |
| CURRENT FILING DATE: 1999-05-28 |
| NUMBER OF SEQ ID NOS: 1 |
| SOFTWARE: PatentIn Ver. 2.1 |
| SOFTWARE: PatentIn Ver. 2.1 |
| SOFTWARE: PATENT OF A SECONDARY CONTROL OF A SECO
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83.3%; Pred. No. 1.4e-218;
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CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/321,589
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 1
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 735
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US-10-293-478-1
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Patent No. 6733757
GENERAL INFORMATION:
APPLICANT: PATEL, SALIL D.
APPLICANT: MCARTHUR, JAMES G.
APPLICANT: MCARTHUR, JAMES G.
FILE REFERENCE: 39672
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Best Local Similarity
Matches 445; Conserv
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Sequence 13. Application US/10038972A

Patent NO. 6962815

GENERAL INFORMATION:

APPLICANT: J. Bartlett

TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US

CURRENT APPLICATION NUMBER: US/10/038,972A

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: US/60/260,124

PRIOR APPLICATION NUMBER: US/80/260,124

PRIOR APPLICATION NUMBER: 08/260,124

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.1

SEQ ID NO 13

LENGTH: 735
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US-10-038-972A-13
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; ORGANISM: adeno-associated virus 2 VP1 caspid protien
US-10-038-972A-13
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Best Local Simi
Matches 445;
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                                                                                                                                                                                                                         LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                                                                                                                                                                            NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                                                                                                                    NGSQAVGRSSFYCLEYFPSQMLRTGNNPTFSYTFBEVPFHSSYAHSQSLDRLMNPLIDQY
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                                                                                                                                                           WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD
                                                                                                                                                                                                     LYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYS
                                        PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                                                    EEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKI
                                                                                                  EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
                                                                                                                                             WTGATKYHLNGRDSLVNPGPAMASHKDDEEKFPPQSGVL1FGKQGSEKTNVD1EKVM1TD
IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                            PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVE
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Pred. No. 1.4e-218;
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RESULT 10
US-09-532-594B-18
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CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FBSLSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 544
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/09532594B Patent No. 6468524
                                                                                                                                                                                                                                                                                                                            APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
OTHER INFORMATION: Description of Artificial OTHER INFORMATION: synthetic construct NAME/KEY: misc_feature OTHER INFORMATION: AAV4 capsid protein VP3
                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                    Sequence; No.
                                                                                      6468524e =
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Query Match
Best Local Similarity 122 239 QYLYYLNRTQN----QSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDN 325; 528 418 358 295 N VTTNDGVTTIANNLTSTVQVFSDSEYQLFYVLGSAHQGCLFPFFADVFMIFQYGY---LT STGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKE ASGGGAPMADNNEGADGYGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISSA 61 NTATVPGTLIFTSEEELAATNATDTDMWGNLPGGDQSNSNLPTVDRLTALGAVPGMVWQN NNSNFTWTGAS---KY----NLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAG GNTSQQQTDRNAFYCLEYFPSQMLRTGNNFEITYSFEKVPFHSMYAHSQSLDRLMNPLID LNNGSQAVGRSSFYCLEYFPSOMLRTGNNFTFSYTFEEVPFHSSYAHSOSLDRLMNPLID ---SLQSNTYNGFSTPWGYFDFNRFHCHFSPRDWQRLINNNWGMRPKAMRVKIFNIQVKE AAAGGAAV-EGGQGADGVGNASGDWHCDSTWSEGHVTTTSTRTWVLPTYNNHLYKRLGE-RYLTHHL 544 RYLTRPL 534 FITQYSTGQVSVEIEWELQKENSKRWNDEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGT RDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKHPPPQIFIKNTPVPANPATTFSSTPVNS RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFAS QNYKIPATGSDSLIKYETHSTLDGRWSALTÞGPPMATAGPADSK-FSNSQLIFAGPKQNG QYLWGLQSTTTGTTLNAGTATTN---FTKLRPTNFSNFKKNWLPGPSIKQQGFSKTA--N VTTSNGETTVANNLTSTVQIFADSSYELPYVMDAGQEGSLPPFPNDVFMVPQYGYCGLVT FITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNYGQQNSLLWAPDAAGKYTEPRAIGT Conservative 58.2%; 65; Score 1690.5; DB 2; Pred. No. 3.1e-146; 5; Mismatches 132; DB 2; Indels Length 544; 25; Gaps 537 347 527 467 417 407 357 298 294 243 238 183 178 123 121 66 477

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GENERAL INFORMATION:
APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THER
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 598
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-532-594B-16
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Best Local Similarity
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                                                                                       FITQYSTGQVSVEIEWELQKENSKRWNDEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGT
                                                                                                                                                 RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFAS
                                                                                                                                                                                                  NTATVPGTLIFTSEEELAATNATUTUMWGNLPGGDQSNSNLPTVDRLTALGAVPGMVWQN
                                                                                                                                                                                                                   ASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQD
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                                                                                                                                                                                                                                                                                           NNSNFTWTGAS---KY----NLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAG
                                                                                                                                                                                                                                                                                                                                 QYLWGLQSTTTGTTLNAGTATTN---FTKLRPTNFSNFKKNWLPGPSIKQQGFSKTA--N
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RYLTHHL 598
                              RYLTRPL 534
                                                                                                                               RDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKHPPPQIFIKNTPVPANPATTFSSTPVNS
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                                                               FITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNYGQQNSLLWAPDAAGKYTEPRAIGT
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Pred. No. 3.6e-146;
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Sequence 4, Application US/09532594B
PAtent No. 6468524
GENERAL INFORMATION:
APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THER
FILE REFERENCE: 14014.025202
CURRENT APPLICATION UNMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 734
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Best Local
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Local Similarity 59.4%; Pred. No. 4.9e-146;
Nes 325; Conservative 65; Mismatches 132;
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RYLTHHL 734
                                                                                                FITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGT
                                                                                                                                              RDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKHPPPQIFIKNTPVPANPATTFSSTPVNS
                                                                                                                                                                 RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFAS
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                                  RYLTRPL 534
                                                                        FITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNYGQQNSLLWAPDAAGKYTEPRAIGT
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LENGTH: 532
TYPE: PRT
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Best Local Simi
Matches 318;
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Patent No. 6855314
GENERAL INFORMATION:
                                               Sequence 5, Application US/09533427 Patent No. 6855314 GENERAL INFORMATION:
APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizab
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OTHER INFORMATION:
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Pred. No. 6
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6.5e-144;
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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
TITLE OF INVENTION: AAV5 VECTOR FOR TRANSDUCING BR.
FILE REFERENCE: 14014.0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23

BRAIN

CELLS

AND LUNG

CELLS

FastSEQ

for Windows Version

US-09-533-427-4

GENERAL INFORMATION:

Sequence 4, Application US/09533427 Patent No. 6855314

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TITLE OF INVENTION: AAVS VECTOR FOR TRANSDUCING BRAIN CELLS AND
FILE REFERENCE: 14014.0323UZ
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 588
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FORGANISM: Artificial Sequence
FEATURE:
FORGANISM: Artificial Sequence
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Best Local
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OTHER INFORMATION:
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                GQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                               PIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYST
                                                                                                                        NMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQEIVPGSVWMERDVYLQG
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GOVTVEMEWELKKENSKRWNPEIOYTNNYNDPOFVDFAPDSTGEYRTTRPIGTRYLTRPL
                                                             PIWAKIPETGAHFHPSPAMGGFGLKHPPPMMLIKNTPVPGN-ITSFSDVPVSSFITQYST
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58.9%;
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Pred. No. 7.6e-144;
4; Mismatches 154;
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LENGTH: 724
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. 6855314e
OTHER INFORMATION: synthetic construct
(S-09-533-427-4)
                                                                                                                                                                                                                                                                                                     Query Match 57.3%; Score 1665; DB 2; Length 724; Best Local Similarity 58.9%; Pred. No. 1e-143; Matches 318; Conservative 54; Mismatches 154; Indels 14;
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                                                                                                                                                                                                                                                    61
                                QYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQF-KNWLPGPCYRQQRVSKTKTDNNNS
                                                                                                                                                                                                 ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                                                                                                                   NFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTAL---D
                                                                                                                                   QYLYRFVSTNNTGGVQFNKNL-----AGRYANTYKNWFPGPMGRTQGWNLGSGVNRAS
                                                                                  414
                                                                                                                                                                                                    372
                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                      252
                 534
                                 664
                                                 474
                                                                  605
                                                                                                   545
                                                                                                                   354
                                                                                                                                   485
                                                                                                                                                    297
                                                                                                                                                                    432
                                                                                                                                                                                                                                                                                      60
 724
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Search completed: November 23, 2005, 17:42:49
Job time: 25.2857 secs